OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Bioacceleration Ltd.

GenCore version 5.1.8

Run on: May 18, 2006, 01:26:43 ; Search time 52 Seconds
(without alignments)
1361.775 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVNKVKPIGENNEN..........PSAEGGEEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SID53/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SID53/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SID53/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SID53/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SID53/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SID53/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SID53/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3166.5	74.8	610	2	US-09-949-016-6945	Sequence 6945, Ap
2	2202	52.0	416	2	US-09-948-016-11669	Sequence 11669, A
3	1949	46.0	909	2	US-09-538-092-1315	Sequence 1315, Ap
4	857	20.2	698	2	US-09-949-016-10215	Sequence 10215, A
5	850	20.1	694	2	US-09-538-092-1351	Sequence 1351, Ap
6	818.5	19.3	690	2	US-09-275-252A-19	Sequence 19, Appl
7	817	19.3	686	2	US-09-538-092-1037	Sequence 1037, Ap
8	817	19.3	694	2	US-09-949-016-11549	Sequence 11549, A
9	655	15.5	575	2	US-09-927-267-1	Sequence 1, Appli
10	640	15.1	575	2	US-09-927-267-16	Sequence 16, Appl
11	484	11.4	261	2	US-09-275-252A-18	Sequence 18, Appl
12	416.5	9.8	256	2	US-09-270-767-46624	Sequence 46624, A
13	413	9.8	1203	2	US-09-949-016-6615	Sequence 6615, Ap
14	413	9.8	1203	2	US-10-067-457-3	Sequence 3, Appli
15	412.5	9.7	910	2	US-08-997-685A-2	Sequence 2, Appli
16	412.5	9.7	910	2	US-09-086-436-31	Sequence 31, Appl
17	412.5	9.7	1109	2	US-09-949-016-10771	Sequence 10771, A
18	405.5	9.6	889	2	US-10-067-457-1	Sequence 1, Appli
19	405.5	9.6	889	2	US-09-949-016-6036	Sequence 6036, Ap
20	399.5	9.4	855	2	US-09-949-016-7263	Sequence 7263, Ap
21	399	9.4	863	2	US-08-997-685A-10	Sequence 10, Appli
22	382.5	9.0	749	2	US-10-067-457-5	Sequence 5, Appli
23	382.5	9.0	749	2	US-09-086-436-39	Sequence 39, Appli
24	382	9.0	528	2	US-09-997-685A-4	Sequence 4, Appli
25	377.5	8.9	504	2	US-09-086-436-33	Sequence 33, Appli
26	370	8.7	597	2	US-08-997-685A-12	Sequence 12, Appli
27	368	8.7	506	2	US-08-997-685A-6	Sequence 6, Appli
28	368	8.7	506	2	US-09-086-436-35	Sequence 35, Appl
29	368	8.7	597	2	US-09-086-436-41	Sequence 41, Appl
30	360.5	8.5	960	2	US-09-694-777A-21	Sequence 21, Appl
31	349	8.2	987	2	US-09-694-777A-22	Sequence 22, Appl
32	347.5	8.2	962	2	US-09-694-777A-24	Sequence 24, Appl
33	345.5	8.2	962	2	US-09-614-480-9	Sequence 9, Appli
34	345.5	8.2	962	2	US-09-694-777A-3	Sequence 3, Appli
35	345.5	8.2	962	2	US-10-422-075-9	Sequence 9, Appli
36	344	8.1	170	2	US-09-358-383C-27	Sequence 27, Appl
37	337	8.0	988	2	US-10-162-012-12	Sequence 12, Appl
38	336	7.9	989	2	US-09-694-777A-23	Sequence 23, Appl
39	335	7.9	988	2	US-09-614-480-2	Sequence 2, Appli
40	335	7.9	988	2	US-10-422-075-2	Sequence 2, Appli
41	335	7.9	988	2	US-09-694-777A-4	Sequence 4, Appli
42	334	7.9	319	2	US-10-358-383C-22	Sequence 22, Appli
43	334	7.9	989	1	US-09-694-777A-4	Sequence 4, Appli
44	317.5	7.5	1159	2	US-08-956-242-13	Sequence 13, Appl
45	317.5	7.5	1159	2	US-09-351-215-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-6945
Sequence 6945, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6945
LENGTH: 610
TYPE: PRT
ORGANISM: Human
US-09-949-016-6945

Query Match 74.8%; Score 3166.5; DB 2; Length 610;
Best Local Similarity 99.0%; Pred. No. 4.3e-272;
Matches 609; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

```
Qy  195 MPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQTADNIHYWL 254
         ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    1 MPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCCFIPLRLVFPYQTADNIHYWL 60

Qy  255 IADIICDIILYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICY 314
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IADIICDIILYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICY 120

Qy  315 LFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACYYYWA 374
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 LFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACYYYWA 180

Qy  375 SNYEGIGTTRWVYDGEGNEYLRCYTWAVRTLITIGGLPEPQTLFEIVFQLINFFSGVFVF 434
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  181 SNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLINFFSGVFVF 240

Qy  435 SSLIGQMRDVIGAATANQNYFRACHDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLD 494
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  241 SSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLD 300
```

```
Qy  495  ESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPLPGDFVCKK  554
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  ESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPLPGDFVCKK  360

Qy  555  GEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFA   614
         |||||||||||||||||||||||||||||||||||      |||||||||||||||||||
Db  361  GEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSV------LLAAGGGNRRTANVVAHGFA   415

Qy  615  NLLTLDKKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLPPKKETPK    674
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  416  NLLTLDKKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLPPKKETPK    475

Qy  675  LFKTLLGGTGKASLARLLKLKREQAAQKKENSEGGEEEGKENEDKQKENEDKG          734
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  476  LFKTLLGGTGKASLARLLKLKREQAAQKKENSEGGEEEGKENEDKQKENEDKG          535

Qy  735  KENEDKDKGRPEEEKPLDRPECTASPIAVEEEEPHSVRRTVLPRGTSRQSLIISMAPSAEG  794
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  536  KENEDKDKGRPEEEKPLDRPECTASPIAVEEEEPHSVRRTVLPRGTSRQSLIISMAPSAEG  595

Qy  795  GEEVLITEVKEKAKQ  809
         |||||||||||||||
Db  596  GEEVLITEVKEKAKQ  610
```

RESULT 2
US-09-016-11669
; Sequence 11669, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11669
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Human
US-09-016-11669

Query Match   52.0%;
Best Local Similarity   99.8%;
  Matches 412; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Score 2202; DB 2; Length 416; Pred. No. 1e-186;

```
Qy  114  PQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV  173
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  PQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV   60

Qy  174  KESDDKPTEHYRLLWFKVKKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLLAYNWNC  233
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  KESDDKPTEHYRLLWFKVKKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLLAYNWNC  120

Qy  234  WFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKH   293
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  WFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKH   180

Qy  294  YRTSTKFQLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRV   353
         ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  YRTSPKFQLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRV   240

Qy  354  IRTTGYLLFILHINACYYYWASNYEGIGTTRWYDGEGNEYLRCYYWAVRTLITIGGLPE    413
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  IRTTGYLLFILHINACYYYWASNYEGIGTTRWYDGEGNEYLRCYYWAVRTLITIGGLPE    300
```

```
Qy  414  PQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPK  473
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  PQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPK  360

Qy  474  LVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFK          526
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  LVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFK          413
```

RESULT 3
US-09-538-092-1315
; Sequence 1315, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

Query Match   46.0%;
Best Local Similarity   46.2%;
  Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps   18;

Score 1949; DB 2; Length 909; Pred. No. 9.8e-164;

```
Qy   14  IGENNENEQSSRRNEEGSHPSNQSQQTTAQE--ENKGE---EKSLKTKSTPVTSEEPHTN   68
         :|:::: :::.. :.  :   :. :::|:|::  ::||:    ::.:: :.:| |.::|
Db   67  VGEEAKKEAEEAKAKEEAEEVAEEEAEKEPQDWAETKEEPEAAEAEAASSGVPATKQHPEVQ  126

Qy   69  IQDK------LSKKNSSGDLTTNPDPQONAAEPTGTVPEQKEMDPGKEGPN------     112
         :.|       ::.: :.||.|.||:| :.||| ||.:||.||:|.:|.||
Db  127  VEDTDADSCPLMAEENPPS--TVLPPSPAKSDTLIVPSSASGTHRKLPSEDDEAEELK     184

Qy  113  -SPQNKP------PAAP------VINEYADAQLHNLVKRMRQRTALY               146
         .||..  :    :    :   :|||||||||||||||||||||
Db  185  ALSPAESVVAWSDPTTKDTDGQDRAASTASTNSAIIND----RLQELVKLFKERTEKV     240

Qy  147  KKKLVEGDLS----SPEASPQTAKPTAVPPVKESDDKPT--EHYYRLLWFKVKKMPLTEY   200
         |:||::. :     ||:||| ::.|.:  :|:.|::||   ||| :|||||||:|.|::|
Db  241  KEKLIDPDVTSDEESPKPSPAKKAPEPAPDTKPAEAEPVEEEHYCDMLCCKFKHRPWKKY    300

Qy  201  LKRIKLPNSIDSYTDRLYLLWLLLVTLLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIIC  260
         |:|: :    ::| ::| :|.|::||:  .:.|:||:|.| .||||||:.||||:||::.|
Db  301  ----QFPQGIDPLTLNMVLWLFFVVMANWNCWLIPVRWAFPYQTPDNIHHWLLMDYLC     356

Qy  261  DIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN   320
         |:||: |: :||.|||||||||||.|.::.:...|:|.|| :|:::   ::|..|:|..
Db  357  DLIYFLDITVFQTRLQFVRGGDIITDKDMRNNYLKSRRFKMDLLSLPLDFLYLKVGVN     416

Qy  321  PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACYYYWASNYEGI   380
         |:.|..| |||::|||||..|||:: ||:.||||||| |||:.||:|:|||||||:|:|
Db  417  PLLRLPRCLKYMAFFEFNSRLESILSKAYVYRVIRTTAYLLYSLHLNSCLYYWASAYQGL    476

Qy  381  GTTRWVYDGEGNEYLRCYYWAVRTLITITGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQ  440
         |:|:||||| ||.|:|||| ||::|:|| ||||:::|||||||||||:|.|||..|::|||
Db  477  GSTHWVYDGVGNSYIRCYYPAVKILITIGGLPDDKTLFEIVFQLLNYFIGVFAAFSVMIGQ  536
```

```
Qy  441 MRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLK 500
        |||:| |||  ||||||:|:| ||||  |   ||||:||||| ||||||||||:||||:::
Db  537 MRDVVGAATAGQTYYRSCMDSTVKXYMNFYKIPKSVQNRVKTWYEYTWHSGGMLDESELMV 596

Qy  501 TLPPTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVVLYLPGDFVCKKGEIGKE 560
        :||  :|||||||||| |:|||:|| ||| |||:|||:||:||| ||| |:||||||||:|
Db  597 QLPDKMRLDLAIDVNYNIVSKVALFQGCDRQMIFDMLKRLRSVVYLPNDYVCKKGEIGRE 596

Qy  561 MYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLD 620
        ||||:  :|||||||||| :|||||||||||||||:|:||||||||||||||||:||| ||
Db  657 MYIIQAGQVQVLGGPDGKSVLVTLKAGSVFGEISLLAVGGGNRRTANVVAHGFTNLLFILD 716

Qy  621 KKTLQEILVHYPDSERIIMKKARVLLKQAKTAEATPPRKDLALLFPPKEETPKLFKTLL 680
        || | ||||||| |::: ||| :|| | :     | |::: || || ||||:| |||::|
Db  717 KKDLNEILVHYPESQKLLRKKAARVMLRSNNK-----PKEEKSVILLPPRAGTPKLFNAAL 771

Qy  681 GGTGKAS------------------------LARLLKLKREQAAQKKENSEGGEEEGKENEDKQKENEDKQK 728
        |                               |:||| :|||  | :|  |  |     |: ||||||||
Db  772 AMTGMGGKGAKGGKLAHLRARLKELALEAAARHEEL---VEQAKSSQDVKGEGGSAAP 828

Qy  729 ENEDKGKE-NEDKDKGREPEEKPLDRPECTASPIAV-----------EEPHSVRRTVLP 776
            :| | :|    |   |  |                          |||||||
Db  829 DQHTHPKEAATDPPAPRTPEPP-GSPPSSPPPASLGSCEGEEEGPAEPEEHSVR----- 882

Qy  777 RGTSRQSLIIISMAPSAEGGEEVLIIEVEKEKAQQ 809
                           |::|  |  |:|:::  |
Db  883 -----------ICMSPGPEPGEQILSVKMPEEREE 906
```

RESULT 4
US-09-949-016-10215
Sequence 10215, Application US/09949016
Patent No. 6812239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10215
LENGTH: 698
TYPE: PRT
ORGANISM: Human
US-09-949-016-10215

Query Match   20.2%; Score 857; DB 2; Length 698;
Best Local Similarity   29.9%; Pred. No. 5.8e-67;
Matches 226; Conservative 153; Mismatches 272; Indels 106; Gaps 22;

```
Qy   19 ENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEEKSLKTKSTPVTSEEPHTNIQDKLSKKNS 78
            :     |||||||||||||||||||||||||||||||||||||||||||||||
Db    1 -----QTEKMAKINTQYSHPS--------RTHLKVK----TSDRDLNRAENGLSRAHS 41

Qy   79 SGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGEGNSPQNKPPAAPVINEYADAQLHNLVKR 138
         | |  :    :  |||:||   |
Db   42 SSEETS-----SVLQP-GIAMETRGLADSGQGSFTGQ----------GIARLSRLIFL 83

Qy  139 MRQRTALYKKKLVEGDLSSP-------EASPQTAKPTAVPPVKESDDKPTEHYYRLLW 189
        :|:||||:||||||||||
Db   84 LRRWAARHVHHQDGQPDSPDRFRGAELKEVSSQESNAQANVGSQEPADRG----RSAW 138

Qy  190 FKVKKMPL-------------------------TEYLKRIKLPNSI-DSYTDRLYLLWLLLLVTLLAYNWNCWFIPL 238
        ||:|||||                          |:|
Db  139 ----PLAKCNTNTSNNTEEEKKTKKKDAIVDPSSNLYYRWLTAIALPVFYNWYLLIC 192
```

RESULT 5
US-09-538-092-1351
Sequence 1351, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1351
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q16281
US-09-538-092-1351

Query Match   20.1%; Score 850; DB 2; Length 694;
Best Local Similarity   30.0%; Pred. No. 2.4e-66;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

```
Qy  239 RLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTST 298
           |     ||:|: |:|||| |  ||||||| :  ||| || |||||:|| |::||: |
Db  193 RACFDELQSEYLMLWLVLDYSADVLYLVDVL-VRARTGFLEQGLMVSDTNRLWQHYKTTT 251

Qy  299 KFQLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFEFNNHLESIMDKAYIYRVIRTI 357
         |:|||      ||  ||  |   ||| ||||| :|:|||: |  | :  ||| ||:  :|
Db  252 QFKLDVULSLVPTDLAYILKVGTNYPEVRFNRLLKFSRLFEFFDRTETRTNYPNMFRIGNLV 311

Qy  358 GYLLIFLIHINACVTYWASNYEGIGTTRWVYDG------EGNEYLRCYWAVRLITIG 409
        || ||  ||:||| :|     |||||| ||| |       ||| | |:|| |:||||
Db  312 LYILIIHWNACIYFAISKFIGFGTDSWVYPNISIPEHGRLSRKYIYSLYWSTLTLTTIG 371

Qy  410 GLPEPQTLFEIVFQLLNFFSGVFVFSSLLIGQMRDVIGAATANQNYFRACMDDTIAYMNNY 469
         :| ::  |:   |:| | |||:|       |::| |||||||||||||||||||||||
Db  372 ETPPVKDEYLFVVVDFLGVLIFATIVGNVGSMISNMNASRAEFQAKIDSIKQYMQFR 431

Qy  470 SIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCD 529
        |||||||||||||||||||||||||||||||||| ||||||||||||| |:|||:|| ||
Db  432 KVTKDLETRVIRWFDYLWANKKTVDEKEVLKSLPDKLKAEIAINVHLDTLKKVRIFQDCE 491

Qy  530 TQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSV 589
        | :: :|:|:| | :| |||:||||| |||||||| ||::| : :|||:| :| |: ||:
Db  492 AGLLVELVLKLRPTVPSPGDYICKKGDIGKEMYIINEGKLAVV-ADDGVTQFVVLSDGSY 550

Qy  590 FGEISLLAAGG--GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERIIMKKAR-VL 645
        ||||| :  |   ||||||| :: | ::| | ||| |||||||||| |   | |:| :|
Db  551 FGEISILNIKGSKSGNRRTANIRSIGYSDLFCLSKDDLMEALTEYPEAKALEEKGRQIL 610

Qy  646 LKQK----AKTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLL-------KL 694
        :|:|     | |::: || || |||| |||:|:| ||||| ||:|| |||:
Db  611 MKDNLIDEELARAGADPKDL------EEKVEQLGSSL--DTLQTFARLLAEYNATQMKM 662

Qy  695 KREQAAQKKENSEGGEE---EGKENEDKQKENEDKQK 728
        |:|:|| ||||| |||    |||||||||:|||||||
Db  663 KQRLSQLESQVKGGGDKPLADGEVPGDATK-TEDKQQ 698
```

```
Qy   87  DPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMRQRTALY 146
             .:                                                 :|
Db   44  ---SVLQP-GIAMETRGLADSGQGSFTGQ---------------------GIARLSRLIFLLRRWAARH 87

Qy  147  KKKLVEGDLSSP------------------EASPQTAKPTAVPPVKESDDKPTEHYYRLIWFKVKKMPL 197
          .||:                         ::|:    |            |     ||:
Db   88  VHHQDQGPSPDRFRGAELKEVSSQESNAQANVGSQEPADRG-----RSAW------PL 136

Qy  198  -------TEYLKRIKLPNSI-DSYTDRLYLLWLLLVTLLAYNWNCWFIPLRLVFPYQT 246
                  |||: |:||   : :  | ||::|:| :: : |   |  :   | :|
Db  137  AKCNTNRSNNTEEEKKTKKKDAIVVDPSSNLYYRWLTAIALPVFYNWYLLICRACFDELQ 196

Qy  247  ADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVAS 306
          ||:||||.||:||| :|:|:||:|||  | ||||||||||||||:||||:||:|:||||
Db  197  SEYLMLWLVDLYSADVLYVLDVL-VRARTGFLEQGLMVSDTNRLWQHYKTTTQFKLDVLS 255

Qy  307  IIPFDICYLFFGFN--PMFRANRMLKYTSFFEENHHLESIMDKAYIYRVIRTTGYLLFLIH 365
          |||:|:|||:|||   ||:||:|||||||||:|||||||:||||||||||||:||||:|:|
Db  256  LVPTDLAYLKVGTNYPEVRFNRLLKFSRLFEFFDRTETRTNYPNMFRIGNLVLYILIIIH 315

Qy  366  INACVYYWASNYEGIGTTRWVYDG-------EGNEYLRCYYWAVRLIITIGGLPEPQTL 417
          :|||:|||:|||||||||||||:|       ||:|||||||||||||||:|:| |||:
Db  316  WNACIYFAISKEIGFGTDSWVYPNISIPEHGRLSRKYIYSLLWSTLLTLTTIGGTPPPVKD 375

Qy  418  FEIVFQLLNFFSGVFVFSSLLGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQK 477
          |||:|||||:|:|:|:||||||||||:|||||:|||||:|||:||||:|||||||||||||
Db  376  EEYLFVVVDFLVGVLIFATIVGNVGSMISNNVASRAEFQAKIDSIKQYMQPRKVTKDLET 435

Qy  478  RVRTWEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDML 537
          |||||||||||||||||||||||||||||||:|||||||||||||:||:|| | :|:|
Db  436  RVIRWFDYLWANKKTVDEKEVLKSLPDKLKAEIAINVHLDTLKKKVRIFQDCEAGLLVELV 495

Qy  538  LRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLA 597
          |||||||||||||||||||||||||||||:||||:|||:|:||::||||||||||||||
Db  496  LKLRPTVFSPGGYICKKGDIGKEMYIINEGKLAVV-ADDGVTQFVVLSDGSYPGEISILN 554

Qy  598  AGG---GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERIIMKKAR---VLLKQK- 650
              |||||||||||||||||||||||||:|||:||::| : :| : |   |:||:
Db  555  IKGSKSGNRRTANIRSIGYSDLFCLSKDDLMEALTEYPEAKKALEEKGRQILMKDNLIDE 614

Qy  651  KTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLL---------KLKREQAAQK 702
          |||||||||||||||||||||||||||||||||||||||||         :|:| :||:
Db  615  ELARAGADPKDI-----EEKVEQLGSSL--DTLQTRFARLLAEYNATQMKMKQRLSQLE 666

Qy  703  KENSEGGEE------EGKENEDKQKENEDKQK 728
          :|:   | |      ||:| :||: |::
Db  667  SQVKGGGDKPLADGEVPGDATK-TEDKQQ 694
```

```
; ORGANISM: Homo sapiens
US-09-275-252A-19

  Query Match        19.3%;  Score 818.5;  DB 2;  Length 690;
  Best Local Similarity   30.0%;  Pred. No. 1.5e-63;
  Matches 221;  Conservative 128;  Mismatches 262;  Indels 125;  Gaps 22;

Qy    5  LTKVNKVKPIGENNENEQSSRRNEEGSHPS------NQSQQTTAQEENKGEE------KSL 53
          :|||                   :||:|: |:  |  :|| :              |||
Db   17  VTMPNVIVP-----DIEKEIRRMENGACSSFSEDDDSAYTSEESENENPHARGSFSYKSL 71

Qy   54  KTKSTPVTSEEPHTNIQDKLSKQNSSGDLITNPEDPQNAAEPTGTVPEQKEMDPGKEGNS 113
          :|  .|    :  :          ::::    |:|||||||||||||||||:||| .
Db   72  R-KGGPSQREQYLPGAIAIFNVNNSS-----NKD----QEPEEKKKKSDDKNE 121

Qy  114  PQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV 173
          |||||||||||||||||||||||||||||||:|||:            ::::
Db  122  NKNDPE----------------------------KKKKKDKERKKK--------- 141

Qy  174  KESDDKPTEHYYRLIWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTL--AYNW 231
          :||||||||||||:||||||||||||||||||:| ::|||:||||||||:|||   |:||
Db  142  EKSKDKKEEHH------------KKEVV---------IDP-SGNTYYNWLFCIILPVMVNW 180

Qy  232  NCWFIPLRLVFPYQTADNIHYWLLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELR 291
          ||||:||||||||||||||||||:|||||||||||||:|| | ||||||||||||||||:
Db  181  T--MVIARACFDELQSDYLEYWLLLDYSDIVLIDM-FVRTRTGYLEQGLLVKELKLI 237

Qy  292  KHYRTSTKFQLDVASIIPFDICYLFFGFN--PMFRANRMLKYTSFFEENHHLESIMDKAYI 350
          |||||||||||||||||||:|:|||:|||   |||||:|||||||:||||||||:||||:|
Db  238  NKYKSNLQFKLDVLSLIPTDLLYFKLGWNYPEIRLNRLLRFSRMFEFFQRTETRTNYPNI 297

Qy  351  YRVIRTTGYLLFLIHINACVYYWASNYEGIGTTRWVY-----DGE---GNEYLRCYYWAV 402
          ||||||||||||:||||:|||:|||:||||||||||      ||    ||:|||||||||
Db  298  FRISNLVMYIVIIIHWNACVFYSISKAIGFGNDTWVYPDINDPEFGRLARKYVVSLLWST 357

Qy  403  RTLIITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLLGQMRDVIGAATANQNYFRACMDDT 462
          ||||:|:|:|:| |||:||:|||||:|::|:|:||||||||||:||||::|||:|||:|||
Db  358  LTLITTIGETPPVRDSEVVFVVVDFLIGVLIFATIVGNIGSMISNMNAARAEFQARIDAI 417

Qy  463  IAYMNNYSIPKLVQKRVRTWEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKV 522
          ||||:|||||||||||||||||||||||||||||||||||||||:||||||||||||:|
Db  418  KQYMHFRNVSKDMEKRVIKWFDYLWTNKKTVDEKEVLKYLPDKLRAEIAINVHLDTLKKV 477

Qy  523  DLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLV 582
          ||:|:|||| :|:||||||||||||||||||||||||||||||:||||:|||:|:|:|||
Db  478  RIFADCEAGLLVELVLKLQPQVVSPGGYICKKGDIGKEMYIIKEGKLAVV-ADDGVTQFV 536

Qy  583  TLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERIIM 639
          ||||||||||||:| ||    ||||||:|:|:|||||||||||||:|||:|::|:::|:|
Db  537  VLSDGSYPGEISILNIKGSKAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLE 596

Qy  640  KKARVLLKQKA----KTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLL--- 692
          |:|:|::||:|    |||||||||||||||||||||||||||||||||||||||||
Db  597  EKGKQILMKDGLLDLNIANAGSDPKDLEEKVTRMEGSVDLLQT------RFARILAEY 648

Qy  693  -----KLKREQAQKK 703
               :|:| :||::
Db  649  ESMQQLKQRLTKVEK 664
```

```

**Left column**

```
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
;
; SEQ ID NO 1037
;   LENGTH: 686
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)..(0)
;   OTHER INFORMATION: Polypeptide Accession Number P29973
US-09-538-092-1037

Query Match   19.3%;   Score 817;   DB 2;   Length 686;
Best Local Similarity   29.9%;   Pred. No. 2e-63;
Matches 226;   Conservative 129;   Mismatches 266;   Indels 136;   Gaps 24;

Qy   5 LTKVNKVKPIGENNENEQSSRRNEEGSHPS-------NQSQQTTAQEENKGEE-------KSL 53
Db   13 VTMPNVIVP-----DIEKEIRRMENGACSSFSEDDDSASTSEESENENPHARGSFSYKSL   67

Qy   54 KTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNS   113
Db   68 R-KGGPSQREQYLPGAIALFNVNNSS-----NKD-----QEPEEKKKKKEKKKKSKSDDKNE 117

Qy 114 PQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV 173
Db 118 NKNDPE--------------------------KKKKKKDKEKKKK--------E   137

Qy 174 KESDDKPTEHYYRLLWFKVKKMPLITEYLKRIKLPNSIDSYTDRLYLLWLLLVTL--AYNW 231
Db 138 EKSKDKEEB-----------KKEVVV-----IDP-SGNTYYNWLFCITLPVMYNW   176

Qy 232 NCWFIPLRLVFPYQTADNIHYWLIADIICDIILYLYDMLFIQPRLQFVRGGDIIVDSNELR 291
Db 177 T--MVIARACFDELQSDYLEYWLILDYVSDIVYLIDM-FVRTRTGYLEQGLLVKEELKLI 233

Qy 292 KHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFEFNNHHLESIMDKAYI 350
Db 234 NKYKSNLQFKLDVLSLIPTDLLYFKLGWNYPEIRLNRLLRFSRMFEFFQRTETRTNYPNI 293

Qy 351 YRVIRTGYLLFLFLHINACVYYWASNYEGIGTTRWVY-----DGE-----GNEYLRCYYWAV 402
Db 294 FRISNLVMYIVIIIIHWNACVFYSISKAIGFGNDTWVYPDINDPEFGRLARKYVYSLYWST 353

Qy 403 RTLIITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDT 462
Db 354 LTLTTIIGETPPVRDSEVVFVVVDFLIGVLIFATIVGNIGSMISNMNARAEFQARIDAI   413

Qy 463 IAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKV 522
Db 414 KQYMHFRNVSKDMEKRVIKWFDYLWTNKKTVDEKEVLKYLPDKLRAEIAINVHLDTLKKV 473

Qy 523 DLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKEIGKEMYIIKHGEVQVLGGPGDGTKVLV 582
Db 474 RIFADCEAGLLVELVLKLQPQVYSPGDYICKKGDIGREMYIIKEGKLAVV-ADDGVTQFV 532

Qy 583 TLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERIM   639
Db 533 VLSDGSYFGEISILNIKGSKAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLE 592

Qy 640 KKARVLLKQKA-----KTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLL--- 692
Db 593 EKGKQILMKDGLLDLNIANAGSDPKDLEEKVTRMEGSVDLLQT------   644

Qy 693 -----KLKREQAAQKK----------ENSEG-GEEEG   713
Db 645 ESMQQKLKQRLTKVEKFLKPLIDTEFSSIEGPGAESG   681
```

**Right column**

```
; Sequence 11549, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 11549
;   LENGTH: 694
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11549

Query Match   19.3%;   Score 817;   DB 2;   Length 694;
Best Local Similarity   29.9%;   Pred. No. 2e-63;
Matches 226;   Conservative 129;   Mismatches 266;   Indels 136;   Gaps 24;

Qy    5 LTKVNKVKPIGENNENEQSSRRNEEGSHPS-------NQSQQTTAQEENKGEE-------KSL  53
Db   21 VTMPNVIVP-----DIEKEIRRMENGACSSFSEDDDSASTSEESENENPHARGSFSYKSL    75

Qy   54 KTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNS   113
Db   76 R-KGGPSQREQYLPGAIALFNVNNSS-----NKD-----QEPEEKKKKKEKKKKSKSDDKNE 125

Qy  114 PQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV  173
Db  126 NKNDPE--------------------------KKKKKKDKEKKKK--------E        145

Qy  174 KESDDKPTEHYYRLLWFKVKKMPLITEYLKRIKLPNSIDSYTDRLYLLWLLLVTL--AYNW 231
Db  146 EKSKDKEEB-----------KKEVVV-----IDP-SGNTYYNWLFCITLPVMYNW       184

Qy  232 NCWFIPLRLVFPYQTADNIHYWLIADIICDIILYLYDMLFIQPRLQFVRGGDIIVDSNELR 291
Db  185 T--MVIARACFDELQSDYLEYWLILDYVSDIVYLIDM-FVRTRTGYLEQGLLVKEELKLI  241

Qy  292 KHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFEFNNHHLESIMDKAYI 350
Db  242 NKYKSNLQFKLDVLSLIPTDLLYFKLGWNYPEIRLNRLLRFSRMFEFFQRTETRTNYPNI  301

Qy  351 YRVIRTGYLLFLFLHINACVYYWASNYEGIGTTRWVY-----DGE-----GNEYLRCYYWAV 402
Db  302 FRISNLVMYIVIIIIHWNACVFYSISKAIGFGNDTWVYPDINDPEFGRLARKYVYSLYWST  361

Qy  403 RTLIITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDT 462
Db  362 LTLTTIIGETPPVRDSEVVFVVVDFLIGVLIFATIVGNIGSMISNMNARAEFQARIDAI   421

Qy  463 IAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKV  522
Db  422 KQYMHFRNVSKDMEKRVIKWFDYLWTNKKTVDEKEVLKYLPDKLRAEIAINVHLDTLKKV  481

Qy  523 DLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKEIGKEMYIIKHGEVQVLGGPGDGTKVLV  582
Db  482 RIFADCEAGLLVELVLKLQPQVYSPGDYICKKGDIGREMYIIKEGKLAVV-ADDGVTQFV  540

Qy  583 TLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERIM   639
Db  541 VLSDGSYFGEISILNIKGSKAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLE  600

Qy  640 KKARVLLKQKA-----KTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLL--- 692
Db  600 VLSDGSYFGEISILNIKGSKAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLE  600
```

RESULT 8
US-09-949-016-11549

```
Db  601  EKGKQILMKDGLLDLNIANAGSDPKDLEEKVTRMEGSVDLLQT-------RFARLIAEY  652
Qy  693  -----KLKREQAAQKK---------ENSEG-GEEEG                          713
Db  653  ESMQQKLKQRLTKVEKFLKPLIDTEFSSIEGPGAESG                         689
```

RESULT 9
US-09-927-267-1
; Sequence 1, Application US/09927267
; Patent No. 6933147
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: CNG2B: A No. 6933147e1 Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 018512-0065100S
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)

US-09-927-267-1

Query Match   15.5%; Score 655; DB 2; Length 575;
Best Local Similarity   29.2%; Pred. No. 3.7e-49;
Matches 165; Conservative 121; Mismatches 241; Indels 38; Gaps 14;

```
Qy  202  KRIKLPNSIDSYTDRLYLLWLLLVTLLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICD  261
Db   19  KARKLLPVLDPSGD--YYVWLNTMVFPVMYNLLILVCRACFPDLQHGYLVAWLVLDYTSD   77

Qy  262  IIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFG-FN   320
Db   78  LIYLLDMV-VRFHTGFELEQGILVVDKGRISSRVVRTWSFFLDLASLMPTDVVVVRLGPHT  136

Qy  321  PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTGYLFLFILHINACVYYWASNYEGI   380
Db  137  PTLRLNRFLRAPRLFEAFDRTETRTAYPNAFRIAKLMLYIFVVIHWNSCLYFALSRYLGF   196

Qy  381  -------NEYLRCYWAVRTLIITIIGGLPEPQTLFEIVFQLLNFFSGVF              432
Db  197  GRDAWVPDPAQPGFERLRQYLYSFYSTLILTTVGDTPPPAREEEVLFMVGDFLLAVM      256

Qy  433  VFSSLIGQMRDVI-GAATANQNYFRACMDDTIA--YMNNYSIPKLVQKRVRTWYEYTWDS   489
Db  257  GPATIMGSMSSVIYNMNTADAAFY---PDHALVKKYMKLQHVNRKLERRVIDWYQHLQIN   313

Qy  490  QRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGGCDTQMIYDMLLRLKSVLYLPGD  549
Db  314  KKMTNEVAILQHLPERLRAEVAVSVHLSTLSRVQIFQNCEASLLEELVLKLQPQTYSPGE   373

Qy  550  FVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGG---GNRRTA   606
Db  374  YVCRKGDIGQEMYIIREGGQLAVV-ADDGITQYAVLGAGLYFGEISIINIKGNMSGNRRTA  432

Qy  607  NNVAHGFANLLTLDKKTLQEILVHYPDSERILMKKAR-VLLK------QKAKTA--EA    655
Db  433  NIKSLGYSDLFCLSKEDLREVLSEYPQAQTIMEEKGREILLKMNKLDVNAEAAEIALQEA   492

Qy  656  TPPRKDLALLFFPKEETPKLFKTLLGGTGKASLARLLKLKREQAAQKK----ENSEGGEE  711
Db  493  TESR--LRGLDQQLDDLQTKFARLLAELESSALKIAYRIERLEWQTREWPMPEDLAEADD   550

Qy  712  EGKENEDKQKENEDKGKE                                            736
Db  551  EGPEPEGTSKDEEGRASQEGPGPE                                      575
```

RESULT 10
US-09-927-267-16
; Sequence 16, Application US/09927267
; Patent No. 6933147
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: CNG2B: A No. 6933147e1 Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 018512-0065100S
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: rat cyclic nucleotide gated cation channel OCNC2

US-09-927-267-16

Query Match   15.1%; Score 640; DB 2; Length 575;
Best Local Similarity   29.1%; Pred. No. 7.8e-48;
Matches 157; Conservative 114; Mismatches 224; Indels 44; Gaps 13;

```
Qy  218  YLLWLLLVTLLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIIYLYDMLFIQPRLQF  277
Db   34  YYVWLNTMVFPIMYNLLIVVCRACFPDLQHSYLVAWFVLDYTSDLLYLLD-IGVRFHTGF    92

Qy  278  VRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFE   336
Db   93  LEQGILVVDKGMIASRYVRTWSFLLDLASLVPTDAAAYVQLGPHIIPTLRLNRFLRVPRLFE 152

Qy  337  FNHHLESIMDKAYIYRVIRTGYLFLFILHINACVYYWASNYEGIGTTRWVYDGEG---    391
Db  153  AFDRTETRTAYPNAFRIAKLMLYIFVVIHWNSCLYFALSRYLGFGRDAWYPDPAQPGFE   212

Qy  392  ---NEYLRCYWAVRTLIITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVI-GA  447
Db  213  RLRRQYLYSFYSTLILTTVGDTPLPDREEEYLFMVGDFLLAVNGFATIMGSMSSVIYNM    272

Qy  448  ATANQNYFRACMDDTIA--YMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTT   505
Db  273  NTADAAFY---PDHALVKKYMKLQHVNKRLERRVIDWYQHLQINKKMTNEVAILQHLPER   329

Qy  506  VQLALAIDVNFSIISKVDLFKGGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIK  565
Db  330  LRAEVAVSVHLSTLSRVQIFQNCEASLLEELVLKLQPQTYSPGEYVCRKGDIGREMYIIR   389

Qy  566  HGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGG---GNRRTANVAHGFANLLTLDKK   622
Db  390  EGGQLAVV-ADDGVTQYAVLGAGLYFGEISIINIKGNMSGNRRTANIKSLGYSDLFCLSKE  448

Qy  623  TLQEILVHYPDSERILMKKAR-VLLK------QKAKTA--EATPPRKDLALLFFPKEE    671
Db  449  DLREVLSEYPQAQAVMEEKGREILLKMNKLDVNAEAAEIALQEATESR--LKGLDQQLDD   506

Qy  672  TPKLFKTLLGGTGKASLARLLKLKR----------EQAAQKKENSEGGEEEGKENEDK    719
Db  507  LQTKFARLLAELESSALKIAYRIERLEWQTREWPMPEDMGEADDEAEPGEGTSKDEGK    565
```

RESULT 11
US-09-275-252A-18
; Sequence 18, Application US/09275252A

```
;       Patent No. 6641997
;       GENERAL INFORMATION:
;       APPLICANT: MacKinnon, Roderick
;       APPLICANT: The Rockefeller University
;       TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
;       TITLE OF INVENTION:  Cation Channel Proteins, Mutant Prokaryotic Cation
;       TITLE OF INVENTION:  Channel Proteins, and Uses Thereof
;       FILE REFERENCE: 018512-0029011US
;       CURRENT APPLICATION NUMBER: US/09/275,252A
;       CURRENT FILING DATE: 1999-03-24
;       PRIOR APPLICATION NUMBER: US 09/045,529
;       PRIOR APPLICATION FILING DATE: 1998-03-20
;       PRIOR APPLICATION NUMBER: US 09/054,347
;       PRIOR APPLICATION FILING DATE: 1998-04-02
;       PRIOR APPLICATION NUMBER: WO PCT/US99/06307
;       PRIOR APPLICATION FILING DATE: 1999-03-22
;       NUMBER OF SEQ ID NOS: 42
;       SOFTWARE: Patentin Ver. 2.1
;
;       SEQ ID NO 18
;       LENGTH: 261
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-275-252A-18

  Query Match             11.4%;  Score 484;  DB 2;  Length 261;
  Best Local Similarity   37.2%;  Pred. No. 1.6e-34;
  Matches  97;  Conservative  58;  Mismatches  94;  Indels  12;  Gaps   4;

Qy     370  VYYWASNYEGIGTTRWVY-----DGE---GNEYLRCYYWAVRTLITIGGLPEPQTLFEIV  421
                             :: || ::       |:| ||| || :| |||:|:| :
Db       1  IIYAISKIGFGVDTWVPNITDPEYGLAREYIYCLYWSTLTLTTIGETPPVKDEEYL      60

Qy     422  FQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTI  481
                  ::| |:| | | |||  | ||:| || || | |||  | | ||:| ||| ||| |
Db      61  FVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKGMEAKVIR  120

Qy     482  WYEYTWDSQRMLDESDLLKTLPTTVQLALALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLK  541
             |:| |  :|  |: |:| ||   | :|| |  | : | |:| ||||  :| |  | |||
Db     121  WFDYLWTNKKTVDEREILKNLPAKLRAEIAINVHLSTLTLKKVRIFHDCEAGLLVELVLKR  180

Qy     542  SVLYLPGDEVCKKGGEIGKEMYIIIKHGEVQVLGGGPDGTKVLVTLKAGSVFGEISILLAAGG-  600
             | : |||  |:|  |||:| |:   : | | | |  |    || || | :  |:    | :
Db     181  PQVFSPGDYICRKQDIGKEMYIIKEGKLAVV-ADDGVTQYALLSAGSCFGEISILNIKGS  239

Qy     601  --GNRRTANVVAHGFANLITL  619
               || ||| | || | ||| 
Db     240  KMGNRRTANIRSLGYSDLFCL  260
```

```
RESULT 12
US-09-270-767-46624
;       Sequence 46624, Application US/09270767
;       Patent No. 6703491
;       GENERAL INFORMATION:
;       APPLICANT: Homburger et al.
;       TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;       FILE REFERENCE: File Reference: 7326-094
;       CURRENT APPLICATION NUMBER: US/09/270,767
;       CURRENT FILING DATE: 1999-03-17
;       NUMBER OF SEQ ID NOS: 6251
;       SOFTWARE: Patentin Ver. 2.0
;
;       SEQ ID NO 46624
;       LENGTH: 256
;       TYPE: PRT
;       ORGANISM: Drosophila melanogaster
;       FEATURE:
;       OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46624

  Query Match             9.8%;  Score 416.5;  DB 2;  Length 256;
  Best Local Similarity   36.8%;  Pred. No. 1.6e-28;
  Matches  78;  Conservative  53;  Mismatches  80;  Indels   1;  Gaps   1;
```

```
Qy     253  WLIADIICDIIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDI  312
                || :  || || |  | | |  | |  |  |:|:|:|| |:|: | :|  |: |:|
Db      45  WLACDFCADIIYLLDVVFFKHRVMYLFEGFWVKNKNLTRKNVMRKLQFKLDLLALLPLEL  104

Qy     313  CYLFGFNPMF-RANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTGYLLFIIHINACVY     371
             |||||||| || |||| || | |: ||:: |   | : | |||||| ||| | ||:|
Db     105  LYFKLGTQAVWLRFRFFKIQSFWEVFRLLDRVISSPHFVRVAKTLTYMLVMIHITAALY  164

Qy     372  YWASNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGV  431
             |||||||||||||| |: |||||||||||||||||||||||||||||||:|||||||||
Db     165  YAYSDYQGLGQNRWVFSGKGHPYVRCFAFATKTATSIGKNPKPERQGEYVFMTVAWLMGV  224

Qy     432  FVFSSLIGQMRDVIGAATANQNYFRACMDDTI  463
             | ||||||||||||||||||||||||||||||
Db     225  FVFALLIGQIRDIISTATRNKHEYRQLEDETL  256
```

```
RESULT 13
US-09-949-016-6615
;       Sequence 6615, Application US/09949016
;       Patent No. 6812339
;       GENERAL INFORMATION:
;       APPLICANT: VENTER, J. Craig et al.
;       TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;       TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;       FILE REFERENCE: CL001307
;       CURRENT APPLICATION NUMBER: US/09/949,016
;       CURRENT FILING DATE: 2000-04-14
;       PRIOR APPLICATION NUMBER: 60/241,755
;       PRIOR APPLICATION FILING DATE: 2000-10-20
;       PRIOR APPLICATION NUMBER: 60/237,768
;       PRIOR APPLICATION FILING DATE: 2000-10-03
;       PRIOR APPLICATION NUMBER: 60/231,498
;       PRIOR APPLICATION FILING DATE: 2000-09-08
;       NUMBER OF SEQ ID NOS: 207012
;       SOFTWARE: FastSEQ for Windows Version 4.0
;
;       SEQ ID NO 6615
;       LENGTH: 1203
;       TYPE: PRT
;       ORGANISM: Human
US-09-949-016-6615

  Query Match             9.8%;  Score 413;  DB 2;  Length 1203;
  Best Local Similarity   23.9%;  Pred. No. 3.5e-27;
  Matches  152;  Conservative  109;  Mismatches  273;  Indels  101;  Gaps  25;

Qy      62  SEEPHTNIQDKLSKKN--SSGDLTTNPD---PQNAAEPTGTVPEQKEMDPGKE------  111
             |:   :   |   |      | |:  ||     |  | | || |:  :| | | :
Db     115  SGSSHGHLHDSAEERRLIAEGDASPGEDRTPPGLAAEPE----------RPGASAQPAASP  165

Qy     112  NSPQNKPPAAPVINEYADAQLHNLVKRMRQRTAL-YKKKLVEGDLSSPEASPQTAKPTAV  170
              |  | |    |: : |   | : | | |  || ||: :|  |:||  |||  | || |
Db     166  PPPQQPPQPRASASCEQPSVD----------TAIKVEGGAAAGDQILPEAEVRLGQAGFM  214

Qy     171  PPVKESDDKPTEHYRLLWFKVKKOMPLTEYLKRIKLPN--SIDSYTD-RLYLLWLLLVTL  227
             || |:   ||| | | |   | ||  | | | |  |:   |:| |:  |: |:|:|| |
Db     215  QRQFGAMLQPGVNKFSLRMFCSQKAVEREQ-ERVKSAGFWIIHPYSDRFY--WDLTMLL  271

Qy     228  AYNNNCWFIPLRLVPPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRG-----G  281
             |     |   | | :    |:  :|| |||  || :||| | |  | | ||      |
Db     272  LMVGNLIIIPVGITF--FKDENTTFMIVFNVVSDFFLIDLV---LNFRTGIVVEDNT  324

Qy     282  DIIVDSNELRKHYRTSTKFQLDVASIIPFDICYL----------------FFGFNPMF  323
              : |:||:|| | ||  |::  |  : |  | |                  | ||| |
Db     325  EIILDPQRIMKYLKSW-FMVDFISSIPVDYIFLIVETRIDSEVYKTARALRIVRFTKIL  383

Qy     324  RANRMLKYTSFFEFNHHLESIMDKAY-----IYRVIRTTGYLLFILHINACVYYWASNYE  378
             |||||| |::| | |:  || |  |      :  : |:||| || || | | |:||:| 
Db     384  SLLRLLRLSRLIRYIHQWEEIFHMTYDLASAAVRIVNLIGMMLLCHWDGCLQFLVPMLQ  443

Qy     379  GIGTTRW-----VYDGEGNEYLRCYYWAVRTLITIG-GLPEPQTLFEIVFQLLNFFSGV  431
             |:| ||       | | |||||||||||||||||| ||||||||||||:||||||||||
Db     444  DFPDDCWVSINNMVNNSWGKQYSYALFKAMSHMLCIGYGROAPVGMSDVWLTMLSMIVGA  503
```

RESULT 14
US-10-067-457-3
Sequence 3, Application US/10067457
Patent No. 6979532
GENERAL INFORMATION:
  APPLICANT: Aventis Pharma Deutschland GmbH
  TITLE OF INVENTION: Process for identifying substances which modulate the
  TITLE OF INVENTION: activity of hyperpolarization-activated cation channels
  FILE REFERENCE: AVE D-2000/A006
  CURRENT APPLICATION NUMBER: US/10/067,457
  CURRENT FILING DATE: 2002-04-09
  PRIOR APPLICATION NUMBER: US/09/779,587
  PRIOR FILING DATE: 2001-02-09
  NUMBER OF SEQ ID NOS: 10
  SOFTWARE: Patentin Ver. 2.1
  SEQ ID NO 3
  LENGTH: 1203
  TYPE: PRT
  ORGANISM: Homo sapiens

Query Match   9.8%; Score 413; DB 2; Length 1203;
Best Local Similarity 23.9%; Pred. No. 3.5e-27;
Matches 152; Conservative 109; Mismatches 273; Indels 101; Gaps 25;

```
Qy   62 SEEPHTNIQDKLSKKN--SSGDLTTNPD---PQNAAEPTGTVPEQKEMDPGKE-----GP 111
           :||:                                                  :GP
Db  115 SGSSHGHLHDSAEERLIAEGDASPGEDRTPFGLAAEPE------RPGASAQPAASP    165

Qy  112 NSPQNKPPAAPVINEYADAQOLHNLVKRMRQRTAL-YKKKLVEGDLSSPEASPQTAKPTAV 170
Db  166 PPPQQPPOPQPASASCEQPSVD--------TAIKVEGGAAAGDQOILPEAEVRLGQAGFM 214

Qy  171 PPVKESDDKPPTEHYYRLLWFKVKKMPLTEYLKRIKLPN--SIDSYTD-RLYLLWLLLVTL 227
Db  215 QROFQPGAMLQPGVNKFSILRMFGSQKAVEREQ-ERVKSAGFWIIHPYSDFRFY--WDLTMLL 271

Qy  228 AYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRG------G 281
Db  272 LMVGNLIIIPVGITF--FKDENTTPWIVFNVVSDTFLIDLV-----LNFRTGIVEDNT 324

Qy  282 DIIVDSNELRKHYRTSTKFQLDVASIIPPFDICYL---------FFGFNPMF 323
Db  325 EIILDPORIKMKYLKSW-FWVDFISSIPVDYIFLIVETRIDSEVYKTARALRIVRFTKIL 383

Qy  324 RANRMLKYTSFEFNHHLESIMDKAY---IYRVIRTTGYLLFILHINACVYYWAGNYE 378
Db  384 SLLRLRLSRLIRYIHQWEEIFHMTYDLASAVRIVNLIGMMLLCHWDGCLQFLVPMLQ 443

Qy  379 GIGTTRW-------VVDGEGNEYLRCYWAVRTLIITIG-GLPEEQTILFEIVFQLLNFPSGV 431
Db  444 DFPDDCWVSINNMVNNSWGKQYSYALFKAMSHNLCIGYGRQPAPVGMSDVWLTMLSMIVGA 503

Qy  432 FVFSSLLIGQMRDVIGAATANQNYFRACMDDTIIAYMNNYSIPKLVQKRVRTWYEYTWDSQR 491
           ::  ::||   .: : : ::|   ||:  ...
Db  504 TCYAMFIGHATALIQSLDSSRRQYQEKYKQVEQYMSFHKLPPDTRQRIHDYYEHRYQG-K 562

Qy  492 MLDESDLLKTLPTTVQLALAIDVNFS---IISKVDLFKGCDTQMIYDMLLRLKSVLYLPG 548
Db  563 MFDEESIIGELSEPLREEI---INFNCRKLVASMPLFANADPNFVTSMLTKLRFEVFQPG 619

Qy  549 DFVCKKGEIGKEMYIIKHGEVQVL-GGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTAN 607
Db  620 DYIIREGTIGKKMYFIQHGVVSVLTKGNKETK----LADGSYFGEICLLTRG---RRTAS 672

Qy  608 VVAHGFANLLTLDKKTLQEILVHYPDSERILMKKA 642
Db  673 VRADTYCRLYSLSVDNFNEVLEEYP----MMRRA 702
```

RESULT 15
US-08-997-685A-2
Sequence 2, Application US/0899768SA
Patent No. 6551821
GENERAL INFORMATION:
  APPLICANT: The Trustees of Columbia University
  APPLICANT: Kandel, Eric
  TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
  FILE REFERENCE: 0575/54806
  CURRENT APPLICATION NUMBER: US/08/997,685A
  CURRENT FILING DATE: 1997-12-12
  NUMBER OF SEQ ID NOS: 60
  SOFTWARE: Patentin version 3.1
  SEQ ID NO 2
  LENGTH: 910
  TYPE: PRT
  ORGANISM: mouse
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (130)..(148)
  OTHER INFORMATION: S1
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (164)..(185)
  OTHER INFORMATION: S2
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (185)
  OTHER INFORMATION: S3
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (208)..(229)
  OTHER INFORMATION: S3
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (243)..(271)
  OTHER INFORMATION: S4
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (291)..(313)
  OTHER INFORMATION: S5
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (332)..(358)
  OTHER INFORMATION: P
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (367)..(387)
  OTHER INFORMATION: S6
  FEATURE:
  NAME/KEY: DOMAIN
  LOCATION: (472)..(602)
  OTHER INFORMATION: CNB
  PUBLICATION INFORMATION:
  DATABASE ACCESSION NUMBER: AAC53518
  DATABASE ENTRY DATE: 1997-12-27
  RELEVANT RESIDUES: (1)..(910)
  US-08-997-685A-2

Query Match   9.7%; Score 412.5; DB 2; Length 910;
Best Local Similarity 20.2%; Pred. No. 2.5e-27;
Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;

```
Db  504 TCYAMFIGHATALIQSLDSSRRQYQEKYKQVEQYMSFHKLPPDTRQRIHDYYEHRYQG-K 562
Qy  492 MLDESDLLKTLPTTVQLALAIDVNFS---IISKVDLFKGCDTQMIYDMLLRLKSVLYLPG 548
Db  563 MFDEESIIGELSEPLREEI---INFNCRKLVASMPLFANADPNFVTSMLTKLRFEVFQPG 619
Qy  549 DFVCKKGEIGKEMYIIKHGEVQVL-GGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTAN 607
Db  620 DYIIREGTIGKKMYFIQHGVVSVLTKGNKETK----LADGSYFGEICLLTRG---RRTAS 672
Qy  608 VVAHGFANLLTLDKKTLQEILVHYPDSERILMKKA 642
Db  673 VRADTYCRLYSLSVDNFNEVLEEYP----MMRRA 702
```

```
Qy   210 IDSYTD-RLYLLMLLLVTLAYNNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDM 268
         |:||      |  |  |  |:||                  | :||   |: |:  |:|
Db   124 HHPYSDFRFY--WDLIMLIMMVGNLVIIPVGITF--FTEQTTTPWIIFNVASDTVFLLDL 179

Qy   269 LFIQPRLQFVRG------GDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYL------ 315
         |:|             :|  |      |:|  |    |:|||    |  |:|
Db   180 I-----MNFRTGTVNEDSSEIILDPKVIKMNYLKSW-FVVDFISSIPVDYIFLIVEKGMD 233

Qy   316 --------PFGFNPMFRANRMLKYTSFFENHHLESIMDKAY------IYRVIRTTGY 359
                       |:|   |     |  |  |    :|          |:| | ||
Db   234 SEVYKTARALRIVRFTKILSLLRLLRLSRLIRYHQWEEIFHMTYDLASAVVRIFNLIGM 293

Qy   360 LFILHINACVYY------WASNYEGIGTTRWYDGEGNEYLRCYYWAVRTLIT 407
         ||:|  :|              :  |     | |:|      | ::  ||:
Db   294 MLLLCHWDGCLQFLIVPLLQDFPDCWVSLNE-----MVNDSWGKQYSYALFKAMSHMLC 347

Qy   408 IG-GLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYM 466
         || |      |  |:|  ||||    | |     :| |||  | ||| :|:    | |
Db   348 IGYGAQAPVSMSDLWITMLSMIVGATCYAMFVGHATALIQSLDSSRRQYEKYKQVEBQYM 407

Qy   467 NNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFS---IISKVD 523
         :  :|    |:   :|     |    : |  |:|  |    | ||  |        |:||
Db   408 SFHKLPADMRQKIHDYYEHRYQG-KIFDEENILSELNDPLREEI---VNFNCRKLVATMP 463

Qy   524 LFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVT 583
         ||     | ||| | :||||: |||| :  || | | |||:|||| |||| ||||::|:|
Db   464 LFANADPNFVTAMLSKLRFEVFQPGDYIIREGAVGKKMYFIQHGVAGVI-----TKSSKE 518

Qy   584 LKA--GSVFGEISLLAAGGNRRTANVVAHGFANLLTLLDKKTLQEILLVHYPDSER----- 636
         |    |:||||| ||  |  :|||:| | ||  |  ||     |: | ||| ::
Db   519 MKLTDGSYFGEICLLTKG---RRTASVRADTYCRLYSLSVDNFNEVLEEYPMRRAFETV 575

Qy   637 ----------ILMKK--------------ARVLLKQKAK------------- 651
                    |||:|                |||||
Db   576 AIDRLDRIGKKNSILLQKFQKDLNTGVFNNQENEILKQIVKHDREMVQAIPPINYPQMTA 635

Qy   652 --TAEATPPRKDL-------------------------------ALLPP----------P 668
            :|||:                                   ||:||         |
Db   636 LNCTSSTTTPTSRMRTQSPPVYTATSLSHSNLHSPSPSTQTPQPSAILSPCSYTTAVCSP 695

Qy   669 KEETPKLFKTLLGGTGKASLARLLKLKREQAAQ----KKENSEGGEEBGKENEDKQKENED 725
         |  :||     |      :  | |  ||  ||     | :|| | |:| :||:|:|:|:||
Db   696 PIQSPLATRTFHYASPTASQLSLMQQPQQOLPQSQVQTQTCTQOQQQQQQQQQQQQQQQQQ 755

Qy   726 KQKENEDKGKENEDKDKGREPEEKPLDRPECTASPIAVEEEPHSVRRTVLPRGTSRQSL- 784
         :: :|::   :|: : :|  |   |     |  | :::    : |    |  :|:|||:
Db   756 QQQQQQQQQQQQQQQQQQPQTPGSSTPKNEVHKSTQALHNTNLTKEVRPLSASQPSLP 815

Qy   785 ------IISMAPSAEGGEEVLTI 801
               ||:| |  ::|||:|:|
Db   816 HEVSTLIS-RPHPTVGESLASI 836
```

Search completed: May 18, 2006, 01:30:02
Job time : 55 secs

This Page Blank (uspto)

OM protein - nucleic search,

Copyright (c) 1993 - 2006 Bioacceleration Ltd.

GenCore version 5.1.8

Run on: May 18, 2006, 23:59:38 ; Search time 588 Seconds
(without alignments)
3861.549 Million cell updates/sec

Title: coding_frame_plus_p2n_model

Perfect score: 4234

Sequence: 1 MFKSLTKVNKVKPIGENNEN..............PSAEGGEEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSWEB_spool/US09855828/runat 17052006_181424_25179/app_query_fasta_1
-DB=issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-HOST=absb02p -USER=US09855828 @CGN_1_1_541 @runat 17052006_181424_25179
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celera_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celera_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celera_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celera_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celera_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celera_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celera_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celera_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celera_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celera_SIDS3/ptodata/2/ina/backfiles1.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3594.5	84.9	2135	3	US-09-949-016-1074	Sequence 1074, Ap
2	3575	84.4	2139	3	US-09-949-016-5798	Sequence 5798, Ap
3	857	20.2	3470	3	US-09-949-016-4344	Sequence 4344, Ap
4	817	19.3	2796	3	US-09-949-016-5678	Sequence 5678, Ap
5	748.5	17.7	32666	3	US-09-949-016-16086	Sequence 16086, A
6	692	16.3	84571	3	US-09-949-016-17420	Sequence 17420, A
7	669.5	15.8	2308	3	US-09-927-267-2	Sequence 2, Appli
8	669	15.8	2366	3	US-09-799-451-351	Sequence 351, App
9	655	15.5	1728	3	US-09-927-267-3	Sequence 3, Appli
10	560	13.2	601	3	US-09-949-016-38930	Sequence 38930, A
11	560	13.2	601	3	US-09-949-016-205286	Sequence 205286,
12	560	13.2	99370	3	US-09-949-016-12816	Sequence 12816, A
13	560	13.2	601	3	US-09-949-016-17540	Sequence 17540, A
14	554	13.1	601	3	US-09-949-016-38931	Sequence 38931, A
15	554	13.1	601	3	US-09-949-016-205287	Sequence 205287,
16	510.5	12.1	996	3	US-09-270-767-15059	Sequence 15059, A
17	416.5	9.8	4276	3	US-09-949-016-4900	Sequence 4900, Ap
18	416.5	9.8	5065	3	US-09-949-016-744	Sequence 744, App
19	416.5	9.8	5065	3	US-10-067-457-4	Sequence 4, Appli
20	412.5	9.7	2733	3	US-10-067-457-2	Sequence 2, Appli
21	406	9.6	3372	3	US-10-067-457-6	Sequence 6, Appli
22	406	9.6	3372	3	US-09-949-016-1392	Sequence 1392, Ap
23	399	9.4	3102	4	US-10-067-457-165	Sequence 165, Appl
24	382.5	9.0	2102	4	US-09-086-436-38	Sequence 38, Appli
25	382.5	9.0	2263	3	US-08-997-685A-9	Sequence 9, Appli
26	382.5	9.0	3224	3	US-08-774-528-238	Sequence 238, App
27	382.5	9.0	3224	3	US-10-120-988-238	Sequence 238, App
28	382	9.0	1584	3	US-08-997-685A-3	Sequence 3, Appli
29	377.5	8.9	1512	3	US-09-086-436-32	Sequence 32, Appl
30	376	8.9	601	3	US-09-949-016-38898	Sequence 38898, A
31	376	8.9	601	3	US-09-949-016-205176	Sequence 205176,
32	371.5	8.8	2976	3	US-09-774-528-317	Sequence 317, App
33	371.5	8.8	2976	3	US-10-120-988-317	Sequence 317, App
34	368	8.7	1518	3	US-09-086-436-34	Sequence 34, Appl
35	368	8.7	1792	3	US-09-086-436-40	Sequence 40, Appl
36	360.5	8.5	3041	3	US-09-694-777A-19	Sequence 19, Appl
37	360.5	8.5	3041	3	US-10-422-075-1	Sequence 1, Appli
38	350.5	8.3	1507	3	US-08-997-685A-5	Sequence 5, Appl
39	349	8.2	3041	3	US-09-694-777A-20	Sequence 20, Appl
40	345.5	8.2	2886	3	US-09-694-777A-13	Sequence 13, Appl
41	345	8.2	3002	3	US-09-694-777A-1	Sequence 1, Appli
42	335	7.9	2967	3	US-09-614-480-1	Sequence 1, Appli
43	335	7.9	2967	3	US-10-162-012-6	Sequence 6, Appli
44	335	7.9	2967	3	US-10-422-075-1	Sequence 1, Appli
45	335	7.9	3553	3	US-10-162-012-4	Sequence 4, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-949-016-1074
Sequence 1074, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1074
LENGTH: 2135
TYPE: DNA
ORGANISM: Human
US-09-949-016-1074

Alignment Scores:
Pred. No.: 0
Score: 3594.50
Percent Similarity: 99.1%
Best Local Similarity: 99.1%
Query Match: 84.9%
DB: 3

Length: 2135
Matches: 690
Conservative: 0
Mismatches: 0
Indels: 5
Gaps: 1

```
US-09-855-828-1 (1-809) x US-09-949-016-1074 (1-2135)

Qy   114  ProGlnAsnLysProProAlaAlaProValIleAsnGluTyrAlaAspGlnLeuHis  133
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CCACAAAACAAACCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACAC  60

Qy   134  AsnLeuValLysArgGlnMetArgThrAlaLeuTyrArgLysArgLysLeuValGluGly  153
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AACCTGGTGAAAAGACAGATGCGTACAGCCCTCTACAGAAAGAGAAAGTTGGTAGAGGGA  120

Qy   154  AspLeuSerSerProGluValAlaSerProGlnThrAlaValProProVal  173
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GATCTCTCCTCACCCGAGGTGGCTTCACCCCAAACTGCAGTTCCACCAGTA  180

Qy   174  LysGluSerAspAspLysProThrGlnHisTyrTyrArgLeuLeuTrpPheLysValLys  193
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AAAGAAAGCGATGATAAGCCAACAACAGCTACTACAGGCTGTTGTGGTTCAAGTCAA  240

Qy   194  LysMetProLeuThrGlnTyrTyrLeuLeuLysProAsnSerIleAspSerTyr  213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  AAGATGCCTTTAACAGAGTACTATTTAAACGAATTAAACAGTATTCCTCACTAC  300

Qy   214  ThrAspArgLeuTyrLeuLeuTrpLeuLeuValThrLeuAlaTyrAsnIleAsnCys  233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  ACAGATCGGCTATACCTCCTGTGGCTCCTTGTCACTCTTGCTTACAATATCAACTGC  360

Qy   234  TrpPheIleProLeuArgLeuValLeuPheProTyrGlnThrArgLeuLeuTrpPhe  253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TGTTTTATACCACTGCGCCTCCGTCTTCCCATATCAAACAACGACTACTGG  420

Qy   254  LeuIleLeuAlaAspIleIleIleCysTyrAspAspMetLeuPheIleGlnPro  273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CTTATTCTCGCAGACATCATAATATGTTATGATGATATGCTATTTATCCAGCCC  480

Qy   274  ArgLeuGlnPheValArgGlyGlyAspSerAsnGluLeuArgLysHis  293
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AGACTCCAGTTTGTAAGGGGAGGACATAATGAGTTGAGGAAACACAC  540

Qy   294  TyrArgThrSerThrLysPheGluGlnLeuAspValAlaSerIleIleIleProPheAspCys  313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TACAGGACTTCTACAAAATTTCAGTTGGAGTGCCATCAATAATACCATTTGATTGC  600

Qy   314  TyrLeuPhePheGlyPheAsnProMetPheArgGlnAlaAsnArgMetLeuLysTyrThrSer  333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TACCTCTTCTTTGGGTTTAATCCAATGTTTAGACGCAAATAGGATGTTAAAGTACACTTCA  660

Qy   334  PhePheGluPheAsnHisHisLeuGluSerIleMetAlaAspLysSerAlaTyrIleTyrArgVal  353
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TTTTTTGAATTTAATCATCACCTAGAGTCTATAATGGACAAAGCATATATATCTACAGAGTT  720

Qy   354  IleArgThrThrGlyTyrLeuLeuPheIleLeuHisIleLeuAsnAlaCysValTyrTyrTrp  373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATTCGAACAACTGGATACTTGCTGTTTATTCTGCACATTAATGCCTGTGTTTATTACTGG  780

Qy   374  AlaSerAsnTyrGluGlyIleLeuGlyTyrThrThrArgTrpValTyrAspGlyIleGlyAsnGlu  393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GCTTCAAACTATGAAGGAATTCTGGGCTACACTACGAGGTGGGTGTATGATGGAATAGGGAATGAA  840

Qy   394  TyrLeuArgCysTyrTyrTyrTyrTyrAlaValAlaArgThrLeuIleThrIleGlyGlyLeuProGlu  413
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TATCTGAGATGTTATTATTATTATTATGCCGGTTGCACTTAATTACCATTGGTGGGCTTCCTGAA  900

Qy   414  ProGlnThrPheLeuPheGlyLeuValLeuAsnPhePheSerGlyValPheVal  433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CCACAAACTTTATTTGAAATTGTTTTTCAACTCTTGAATTTTTTTTCTGGAGTTTTTGTG  960

Qy   434  PheSerSerSerLeuIleGluGlyIleGlnMetArgAspValIleGlyAlaAlaThrAlaAsnGlnAsn  453
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTCTCCAGTTTAATTGGTCAGATGAGGGATGTGATTGGAGCAGCTACAGCCAATCAAAAC  1020

Qy   454  TyrPheArgAlaCysSerMetAspAspThrIleAlaTyrMetAsnAsnTyrSerIleProLys  473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  TACTTCCGCGCCTGCATGGGATGACACCATTGCCTACATGAACAATTACTCCATTCCTAAA  1080
```

```
Db  1021  TACTTCCCGCCTGCATGGATGACACCATTGCCTACATGAGCATTACTCCATTCCTAA  1080

Qy   474  LeuValGlnIleLysArgValArgGlnThrArgGlnThrTyrGlnTyrThrArgAspSerGlnAsnArgMetLeu  493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  CTTGTGCAAAAGGCGAGTTCGGAGCTGGTTATGGAAATATACATGGAACTT  1140

Qy   494  AspGluSerAspLeuLeuLeuLysThrLeuProThrThrThrValGlnLeuAlaLeuAlaIleLeuAspAsp  513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GATGAGTCTGATTTGCTTAAGACCCTACCAACTACAGGTTCAGTTCAGCCTTAGCCCCTCGCCAA  1200

Qy   514  ValAlaAsnPheSerIleIleIleSerGluSerValValAlaAspLeuProLysProPheGlyLysCysAsp  533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GTGAAACTTCAGCAATCATCAGCAAAGTCCGACTTGTTCCAAGGGTTGTGATACACAGATGATT  1260

Qy   534  TyrAspMetLeuLeuArgLeuGluLeuTyrSerValLeuTyrLeuProGlyAspPheValCysLys  553
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TATGACATGTTGCTAAGATTGAAATCCGTTGCTTATTTGCCTGGAGACTTTGTCTGCAAA  1320

Qy   554  LysGlyGlyIleLeuGluGlyLysGluMetTyrIleIleLeuLysLysHisSerTyrProAsp  573
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AAGGGAGGAAATTGGCAAGGAAAAGTTATATCATCAAGCATAGCCCAACGTTCCCAGA  1380

Qy   574  GlyProAspProGlyTyrThrLysTysValLeuValAlaThrLeuLeuLysSerAlaLysSerThrAla  593
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  GGCCCTGATGGTACTAAAGTTCTGGTTGTCACTCTCAAAAGTGCAAAAAGTACAGCA  1428

Qy   594  SerLeuLeuAlaIleAlaGlyTyrGlyValGlyAsnArgArgThrAlaAsnValAlaValAlaAlaHisGlyPhe  613
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1429  ---CTTCTAGCACGGAAGGGAGTTGGAGTTGGGAACAGCAGAACTGCCAATGTGGCCCCACGGGTTT  1485

Qy   614  AlaAsnLeuLeuThrThrLeuAspLysTyrIleLeuIleLeuGluValHisIleTyrProAsp  633
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1486  GCCAATCTTTTAACTACTCTAGACAAATATATCAGAAAGTTCATTATTCCAGAT  1545

Qy   634  SerGluArgIleLeuGluMetLysLysLysSerAlaAlaArgValLeuLeuLeuLysGlnLysSerThrAla  653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1546  TCTGAAAGGATCTTCATGAAGAAAAGCCAGAGTGCTTTTAAGCAGAAGGCTAAGACCGCA  1605

Qy   654  GluAlaThrProProArgGlyLysAspLeuAsnLeuAlaLeuLeuPheProProLysGluGluProGluThrPro  673
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1606  GAAGCAACCCCTCCAAGAAAAGACTTGCCCTCCTCCAAAGAAGAGCACACCC  1665

Qy   674  LysLysLeuPheGluLysSerThrLeuArgThrGlyLysLysSerAlaSerLeuAlaArgLeuLeuLysLys  693
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1666  AAACTGTTTTAAAAATCTCCCTAGGGACGGAGAAAAGAAAGCCACAGTCTTGCAAGACTACTCAA  1725

Qy   694  LeuLysLysArgGlyGlnIleAlaLeuAlaGlyIleLysLysLysLysLysValGlyLysGlyGly  713
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1726  TTGAAGCAGCAAGCACCTCAGATAGCTCTAGCAGGAATTAAAAAGAAAAAGAAGGAAGGA  1785

Qy   714  LysGluGluAsnGluGluProLysLysSerGlyAsnGluAsnGluGluLysGluAsnGluGluAsnAspLys  733
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1786  AAAGAAGAAAATGAAGAGCCAAAGAAATCAGGCAATGAAAATGAAGAAAAAGAAAATGAAGAGAATAAA  1845

Qy   734  LysGluGluAsnGluAspLysArgGlyLysAsnGluAsnGluGluProLeuAspArg  753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1846  GGAAAAGAAAATGAAGATAAAAGAGGAAGAAAATGAAGAACCACTGGACAGA  1905

Qy   754  ProGluCysThrAlaSerProIleAlaValGlyLeuGluProHisSerSerValAlaArgGlyThr  773
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1906  CCTGAATGTACAGCAAGTCCTATTGCAGTTGGGCTGGAGCCCCACTCCAGTGTAGCAAGAGGACA  1965

Qy   774  ValLeuProArgGlyThrSerArgGlnSerLeuIleIleIleSerMetAlaProSerGlnGlu  793
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1966  GTTTTACCCAGAGGGACTTCTCGTCAATCACTCATTATCATCTCCATGGCTCCTTCTCAGGAG  2025

Qy   794  GlyGlyLysGluValLeuValAllLysGlyLysAlaLysGln  809
              |||||||||||||||||||||||||||||||||||||||||
Db  2026  GGCGGGAAGGAAGTTCTTACTATTGAAGTCAAAAGAAAAAGGCTAAGCAA  2073
```

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5798
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5798

Alignment Scores:
Pred. No.:
Score: 3575.00
Percent Similarity: 98.9%
Percent Identity: 98.9%
Best Local Similarity: 84.4%
Query Match: 84.4%

Length: 2139
Matches: 690
Conservative: 0
Mismatches: 0
Indels: 1
Gaps: 7
                     2

US-09-855-828-1 (1-809) x US-09-949-016-5798 (1-2139)

Qy   114 ProGlnAsnLysProProAlaAlaProValIleAsnGluThrArgIleAlaAspAlaGlnLeuHis 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   CCACAAAACAAACCGCCTGCAGCTCCTGTTATAAATGACTATGGCGATCCCAGCTACAC 60

Qy   134 AsnLeuValLysArgMetArgGlnArgThrAlaLeuTyrLysLysLysLeuValGluGly 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   AACCTGGTCAAAAGAATGCGGTCAAAGAACCAGCCCCTCACAAGAAAAAAGTTGGTAAGGGA 120

Qy   154 AspLeuSerSerProGluValAlaSerProGlnThrAlaLysProThrAlaValProProVal 173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATCTCTCCTCACCCGAGGCACCACCCAAACCTACAAAGCCCACGGACGTGTACCCACAGTA 180

Qy   174 LysGluSerAspsProThrGluHisTyrArgTyrArgLeuLeuTrpPheLysValLys 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGAAAGCGATGATAAGGCAACAAGACAATTACTACAGGCGTCGTTGTGGTTCAAAGTCAAA 240

Qy   194 LysMetProLeuThrGluTyrTyrLeuTyrArgIleLysLeuProAsnSerIleAspSerTyr 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGATGCCCTTAACAGAGTACTTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATAC 300

Qy   214 ThrAspAspArgLeuLeuTrpLeuLeuValThrLeuAlaThrTyrAsnTrpAsnCys 233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACAGATCGACTCTTATCCTCCTGGCTCTTGCTGTCACTCACTTCAAACTGGAACTGC 360

Qy   234 TrpPheIleProLeuArgLeuValPheProTyrGlnThrAlaAspAsnIleHisTyrArgTrp 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TGGTTTATACCACTGCGCCCTCGTTCCCATATCAGACACAACTACACTTGG 420

Qy   254 LeuIleLeuAlaAspIleLeuCysAspIleLeuTyrLeuTyrAspMetLeuPheIleGlnPro 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCC 480

Qy   274 ArgLeuLeuGlnProValArgGlyGlyGlyAspSerAsnGluLeuArgLysHis 293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGACTCCAGTTGTTGAAGGAGACATAATGAGTTAAGGAAAACAC 540

Qy   294 TyrArgThrSerThrLysPheGlnLeuAspValAlaSerIleIleLeuProPheAspIleCys 313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TACAGGACTTCTCCAAAATTTCAGTTGGATGTCGCCATCAATAATACCATTTGATAATTGC 600

Qy   314 TyrLeuPhePheGlyPheAsnProMetPheArgAlaAsnArgMetLeuLysTyrThrSer 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TACCCTCTTCTTGGGTTTAATCCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCA 660

Qy   334 PhePheGluPheAsnHisSerLeuGluSerIleMetAspGlyAlaIleTyrIleTyrArgVal 353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TTTTTTGAATTTAATCATCACCTAGAGTCTATAAATGACAAAGCAATATCTACAGAGTT 720

Qy   354 IleArgThrThrGlyTyrArgLeuLeuPheIleIleLeuHisSerIleAsnAlaCysValThrTyrTyrTrp 373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTCGAACAACTGGATACTTGCCTGTTTATTCTGCACATTAAATGCCTGTGTTTATACTGG 780

Qy   374 AlaSerAsnTyrGluGlyIleGlyTyrTrpArgTrpValTyrAspGlyGlyGlyAsnGlu 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCTTCAAACTATGAAGGAATTGGCTACTGGAGATGGGTGTATGATGGGGGAAACGAG 840

Qy   394 TyrLeuArgGlyTyrTyrTyrProAlaValArgThrLeuIleThrIleThrLeuProGlu 413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TATCTCAGAGTTATTATTACTGGCAGTTCGAACTTTAATTACCATTGGTGGGCCTTCCAGA 900

Qy   414 ProGlnThrLeuPheGluIleValPheGluGlnLeuLeuAsnPhePheSerGlyValPheVal 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCACAAACTTTATTTGAAATTGTTTTTGAACTCTTGAATTTTTTTCTGGAGTTTTTGTG 960

Qy   434 PheSerSerLeuIleGlyGlnMetArgAspValIleGlyAlaAlaAlaThrAlaAsnGlnAsn 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTCTCCAGTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTGCTACAGCCAATCAGAAC 1020

Qy   454 TyrPheArgAlaCysMetAspAspAspThrIleAlaTyrMetAsnAsnTyrSerIleProLys 473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TACTTCCGCGCCTGCATGGATGACGACACCATTGCCTACATGAACAATTACTCCATTCCTAAA 1080

Qy   474 LeuValGlnIleLysArgValAlaArgGlyThrGlyTyrGluTyrThrTrpAspSerGlnAsnArgMetLeu 493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTTGTGCAAATCAAGCGAGTTGCGAGAGGGACTGGTTATGAATATACAATGGGACTCTCAAAGAATGCTA 1140

Qy   494 AspGluSerAspLeuLeuLysLeuTyrSerThrLeuProThrThrHisValGlnLeuLeuAlaIleLeuAsp 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGAGTCTGATTTGCTTAAGCTCTATAGCACCCTACCAACTACGCCTCCAGTTAGCCCTGCCATTGAT 1200

Qy   514 ValAsnPheSerIleIleSerLysValAlaAspLeuPheLys---GlyCysAspThrGlnMe 532
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1201 GTGAACTTCAGCATCATCAGCAAAGTCGACTTGTTCAAGGGCTGTGTGATACACAGAT 1260

Qy   532 tIleTyrArgAspMetLeuLeuArgLeuLeuLysSerValLeuTyrLeuProGlyGlyAspPheValCy 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATTTATGACATGTTGCTAAGATTGTAAAATCCGTTCTATTGCCTGGTGACTTTGTCTG 1320

Qy   552 sLysLysGlyGlyIleLeuIleLeuGlyLysGluMetTyrIleLeuGlyValGlnValIle 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CAAAAAGGGAGAAATTCTGATCCTAGGGAAAGAAATGTATATCATCAAGGCATGGAAGTCCAAGTTCT 1380

Qy   572 uGlyGlyProAspGlyThrGlyValValLeuValThrLeuuValAlaGlySerValPheGlyGl 592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGCCCTGATGGGTACTGAAGTTCTGGTTACTCTGAAAGCTGGGTCGGTC------ 1432

Qy   592 uIleSerLeuLeuuAlaAlaGlyGlyAsnArgArgThrAlaAsnValAlaAlaHisGl 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 ------CTTCTAGCAGCAGGGGAGGAAACCGTGGAACTGCCAAATGTGGTCGCACGG 1485

Qy   612 yPheAlaAsnLeuLeuThrLeuAspLysLysThrLeuGlnIleLeuuLeuValHisTyrPr 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 GTTTCCAATCTTTTAACCTCTAGACAAAAGACCCTCCAAGAAATTCTAGTGCATTATCC 1545

Qy   632 oAspSerGluArgIleLeuMetLysLysValAlaArgValLeuLeuLysGlnLysSerAlaLysTh 652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 AGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTAAAGCAGAAGTCTGCTAAGAC 1605

Qy   652 rAlaGluValAlaThrProProArgLysAspLeuuAlaLeuLeuProProLysGlyGluTh 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 CGCAGAAGCAACCCCTCCAAGAAAAGATCTTGCCCTCCTTCCACCGAAAAGAGAGAC 1665

Qy   672 rProLysLeuPheLysThrLeuuGlyThrGlyLysGlyAlaSerLeuAlaArgLeuuLe 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db       1666 ACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAAAGCAAGTCTTGCAAGACTACT 1725

Qy        692 uLysLeuLysArgGluGlnAlaAlaGlnLysLysGluAsnSerGluGlyGlyGluGluGl 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 CAAATTGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAAATTCTGAAGGAGGAGAGGAAGA 1785

Qy        712 uGlyLysGluAsnGluAspLysGlnLysGluAsnGluAspLysGlnLysGluAsnGluAs 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 AGGAAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGA 1845

Qy        732 pLysGlyLysGluAsnGluAspLysAspLysGlyArgGluProGluGluLysProLeuAs 752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 TAAAGGAAAAGAAAATGAAGATAAAGATAAAGGAAGAGAGCCAGAAGAGAAGCCACTGGA 1905

Qy        752 pArgProGluCysThrAlaSerProIleAlaValGluGluGluProHisSerValArgAr 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 CAGACCTGAATGTACAGCAAGTCCTATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAG 1965

Qy        772 gThrValLeuProArgGlyThrSerArgGlnSerLeuIleIleSerMetAlaProSerAl 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 GACAGTTTTACCCAGAGGGACTTCTCGTCAATCACTCATTATCAGCATGGCTCCTTCTGC 2025

Qy        792 aGluGlyGlyGluGluValLeuThrIleGluValLysGluLysAlaLysGln 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 TGAGGGCGGAGAAGAGGTTCTTACTATTGAAGTCAAAGAAAAGGCTAAGCAA 2077

RESULT 3
US-09-949-016-4344
; Sequence 4344, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4344
;   LENGTH: 3470
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-4344

Alignment Scores:
Pred. No.:              2.79e-85        Length:         3470
Score:                  857.00          Matches:        226
Percent Similarity:     50.1%           Conservative:   153
Best Local Similarity:  29.9%           Mismatches:     272
Query Match:            20.2%           Indels:         106
DB:                     3               Gaps:           22

US-09-855-828-1 (1-809) x US-09-949-016-4344 (1-3470)

Qy         19 GluAsnGluGlnSerSerArgArgAsnGluGluGlySerHisProSerAsnGlnSerGln 38
              :::   |||:::   ::::::   |||   :::   ||||||||||||
Db         28 CAAACCGAGAAGATGGCCAAGATCAACACCCAATACTCCCACCCCTCC------------ 75

Qy         39 GlnThrThrAlaGlnGluGluAsnLysGlyGluGluLysSerLeuLysThrLysSerThr 58
                                                        ||||||   |||
Db         76 ---------------------------------AGGACCCACCTCAAGGTAAAG------ 96

Qy         59 ProValThrSerGluGluProHisThrAsnIleGlnAspLysLeuSerLysLysAsnSer 78
                    ||||||:::                  ::::::   ||||||:::   :::|||
Db         97 ------ACCTCAGACCGAGATCTCAATCGCGCTGAAAATGGCCTCAGCAGAGCCCACTCG 150

Qy         79 SerGlyAspLeuThrThrAsnProAspProGlnAsnAlaAlaGluProThrGlyThrVal 98
              |||   :::   |||:::               :::      :::|||   |||
Db        151 TCAAGTGAGGAGACATCG---------------TCAGTGCTGCAGCCG---GGGATCGCC 192

Qy         99 ProGluGlnLysGluMetAspProGlyLysGluGlyProAsnSerProGlnAsnLysPro 118
                 |||   :::   :::            :::|||      :::   |||
Db        193 ATGGAGACCAGAGGACTGGCTGACTCCGGGCAGGGCTCCTTCACCGGCCAG--------- 243

Qy        119 ProAlaAlaProValIleAsnGluTyrAlaAspAlaGlnLeuHisAsnLeuValLysArg 138
                                               |||:::|||      |||:::
Db        244 ---------------------------GGGATCGCCAGGCTGTCGCGCCTCATCTTCTTG 276

Qy        139 MetArgGlnArgThrAlaLeuTyrLysLysLysLeuValGluGlyAspLeuSerSerPro 158
              :::|||:::      |||   :::               :::|||      |||   |||
Db        277 CTGCGCAGGTGGGCTGCCAGGCATGTGCACCACCAGGACCAGGGACCGGACTCTTTTCCT 336

Qy        159 ---------------------------GluAlaSerProGlnThrAlaLysProThrAla 169
                                         |||   |||   |||   :::         |||
Db        337 GATCGTTTCCGTGGAGCCGAGCTTAAGGAGGTGTCCAGCCAAGAAAGCAATGCCCAGGCA 396

Qy        170 ValProProValLysGluSerAspAspLysProThrGluHisTyrTyrArgLeuLeuTrp 189
                          :::|||      |||:::                  |||      |||
Db        397 AATGTGGGCAGCCAGGAGCCAGCAGACAGAGGG---------------AGAAGCGCCTGG 441

Qy        190 PheLysValLysLysMetProLeu------------------------------ThrGlu 199
                                ||||||                              ||||||
Db        442 ------------------CCCCTGGCCAAATGCAACACTAACACCAGCAACAACACGGAG 483

Qy        200 TyrLeuLysArgIleLysLeuProAsnSerIle---AspSerTyrThrAspArgLeuTyr 218
                    |||:::   |||      ::::::|||            :::      ||||||
Db        484 GAGGAGAAGAAGACGAAAAAGAAGGATGCGATCGTGGTGGACCCGTCCAGCAACCTGTAC 543

Qy        219 LeuLeuTrpLeuLeuLeuValThrLeuAlaTyrAsnTrpAsnCysTrpPheIleProLeu 238
                    ||||||      :::   |||         :::|||   :::   :::
Db        544 TACCGCTGGCTGACCGCCATCGCCCTGCCTGTCTTCTATAACTGGTATCTGCTTATTTGC 603

Qy        239 ArgLeuValPheProTyrGlnThrAlaAspAsnIleHisTyrTrpLeuIleAlaAspIle 258
              |||      |||            ::::::   :::      ||||||:::   |||
Db        604 AGGGCCTGTTTCGATGAGCTGCAGTCCGAGTACCTGATGCTGTGGCTGGTCCTGGACTAC 663

Qy        259 IleCysAspIleIleTyrLeuTyrAspMetLeuPheIleGlnProArgLeuGlnPheVal 278
                    |||::::::|||:::   |||:::|||   ::::::   |||      |||:::
Db        664 TCGGCAGATGTCCTGTATGTCTTGGATGTGCTT---GTACGAGCTCGGACAGGTTTCTC 720

Qy        279 ArgGlyGlyAspIleIleValAspSerAsnGluLeuArgLysHisTyrArgThrSerThr 298
                    |||   ::::::   |||:::|||   |||   :::||||||:::|||:::|||
Db        721 GAGCAAGGCTTAATGGTCAGTGATACCAACAGGCTGTGGCAGCATTACAAGACGACCACG 780

Qy        299 LysPheGlnLeuAspValAlaSerIleIleProPheAspIleCysTyrLeuPhePheGly 318
              :::|||:::|||||||||   |||::::::|||   |||:::   ||||||      |||
Db        781 CAGTTCAAGCTGGATGTGTTGTCCCTGGTCCCCACCGACCTGGCTTACTTAAAGGTGGGC 840

Qy        319 PheAsn---ProMetPheArgAlaAsnArgMetLeuLysTyrThrSerPhePheGluPhe 337
                 |||   |||      |||   ||||||:::||||||::::::      |||||||||
Db        841 ACAAACTACCCAGAAGTGAGGTTCAACCGCCTACTGAAGTTTTCCCGGCTCTTTGAATTC 900

Qy        338 AsnHisHisLeuGluSerIleMetAspLysAlaTyrIleTyrArgValIleArgThrThr 357
                          |||:::      :::         ::::::|||:::
Db        901 TTTGACCGCACAGAGACAAGGACCAACTACCCCAATATGTTCAGGATTGGGAACTTGGTC 960

Qy        358 GlyTyrLeuLeuPheIleLeuHisIleAsnAlaCysValTyrTyrTrpAlaSerAsnTyr 377
                 |||:::|||   |||:::|||   |||||||||:::|||:::      |||   :::
Db        961 TTGTACATTCTCATCATCATCCACTGGAATGCCTGCATCTACTTTGCCATTTCCAAGTTC 1020

Qy        378 GluGlyIleGlyThrThrArgTrpValTyrAspGly------------------------ 389
                 |||   ||||||      |||||||||
Db       1021 ATTGGTTTTGGACAGACTCCTGGGTCTACCCAAACATCTCAATCCCAGAGCATGGGCGC 1080

Qy        390 GluGlyAsnGluTyrLeuArgCysTyrTyrTrpAlaValArgThrLeuIleThrIleGly 409
                       :::|||:::         ||||||:::      ||||||   |||||||||
Db       1081 CTCTCCAGGAAGTACATTTACAGTCTCTACTGGTCCACCTTGACCCTTACCACCATTGGT 1140

Qy        410 GlyLeuProGluProGlnThrLeuPheGluIleValPheGlnLeuLeuAsnPhePheSer 429
```

Alignment Scores:
Pred. No.:
Score: 817.00
Percent Similarity: 46.9%
Best Local Similarity: 29.9%
Query Match: 19.3%

Length: 2796
Matches: 226
Conservative: 129
Mismatches: 266
Indels: 136
Gaps: 24

US-09-855-828-1 (1-809) x US-09-949-016-5678 (1-2796)

Qy   5 LeuThrLysValAsnLysValLysProIleGlyGluAsnAsnGluAsnGlnSer 24
              ||||:|| ::: ||:::
Db   365 GTAACCATGCCCAATGTGAATGATTGTACCA----------GATATTGAAAAGAAATA 409

Qy   25 ArgArgAsnGluGluGlyGlySerHisProSer--------------AsnGlnSerGlnThr 40
              ||||| |::| :::
Db   410 CGAAGGATGAGAAAAATGGAGCATGCAGCTCCTTTTCTGAGGATGAGAGTGCCTCTACA 469

Qy   41 ThrAlaGlnGluGluAsnGlyGlyGluGlu----------------LysSerLeu 53
              |||||||| |||
Db   470 TCTGAAGAATCAGAGAATGAAAAACCCTCATGCAAGGGGTTCCTTTAGTGTTATAAGTCACTC 529

Qy   54 LysThrLysSerThrProValThrSerGluGluProHisThrAsnIleGlnAsnAspLysLeu 73
                 ||::: ||||::
Db   530 AGA----AAGGGAGGGACCACATCACAGAGGCAGTAACCTGCCTGGGCTCCCATTGCACTTTT 586

Qy   74 SerLysLysAsnSerSerGlyAspLeuThrThrAsnProAsnProGlnAsnAlaAlaGlu 93
              ||||||| ||||
Db   587 AATGTGAACAACAGCAGC----------------------------------AATAAGGAC 619

Qy   94 ProThrGlyThrValProGluGlnLysGluMetAspProGlyLysGluGlyProAsnSer 113
              ||| ::::
Db   620 CCAGAAGGAAAAAGAAAGAAAGAAAGAGAGAAGAGAGCAAGTCAGATGATAAAAACGAA 679

Qy   114 ProGlnAsnLysProProAlaAlaProValIleLeuAsnGluTyrAlaAspAlaGlnLeuHis 133
                 ||||||||
Db   680 AATAAAAAAACGACCCAGAG 697

Qy   134 AsnLeuValLysArgMetArgGlnThrAlaLeuTyrLysLysGlyLeuValGluGly 153
              :::|::: ||||:|||
Db   698 ------------------AAGAAAGAGAAGAAAAGGACAAAAGAGAGAAAAGAA 736

Qy   154 AspLeuSerSerProGluAlaSerProGlnThrAlaLysProThrAlaValProProVal 173
              ||| ||||
Db   737 ---------------------------- 737

Qy   174 LysGluSerAspAspLysProThrGluHisTyrTyrArgLeuLeuTrpPheLysGlyValLys 193
              :::::::||| ||||||
Db   740 GAGAAAAGCAAAGATAAGAAAAAGAGAGAG------------------------AAG 772

Qy   194 LysMetProLeuThrGluTyrLeuLysArgIleLysProAsnSerIleLeuAspSerTyr 213
              || ||||
Db   773 AAAGAAGTTGTGGTT---------------------------------ATTGATCCC--- 796

Qy   470 SerIleProLysLeuLeuValGlnGlnLysArgValArgArgThrTrpTyrGluTrpAspSer 489
              ::: ||:|:
Db   1261 GCCTCACGGCACGAGTTCCAGGCCCAAGATTGATTCCATCAAGAGACTACATGCAGTTCCGC 1320

Qy   490 GlnArgMetLeuAlaSerAspGluSerAspLeuLeuLysThrLeuProThrThrValGlnIleLeuAla 509
              ::: ||::
Db   1321 AAGGTCACCAAGGACTTGGAGACGGGGTTTATCCGGGTGTTTGACTACCTGTGGGCCAAC 1380

Qy   510 LeuAlaIleAlaAspValAsnPheSerIleIleLeuSerGluSerIleLeuGlyGlnCysAsp 529
              ||||| ||
Db   1381 AAGAAGACGGTGGATGAGAAAGGAGGAGTTGCTCAAGAGAGCATCCTTGGCCAGTGCGAC 1440

Qy   530 ThrGlnMetIleTyrAspMetLeuLeuArgGlnLeuTyrLeuProGlyAsp 549
              :::|:|| ||||::|||
Db   1441 ATCGCCATCAACGTGCACCTGGACGCTGAGAAGGTTCGCATCTTCCAGGAC 1500

Qy   550 PheValCysLysLysGlyGluIleGluLysGlyGlnMetTyrIleIleLeuLeuHisGlyGluVal 569
                 ::: |::|
Db   1501 GCAGGGCGTGGCTGGGACGCTGGGGTCTGAAGCTGCGACCCCATGCTTGGGGAT 1560

Qy   570 GlnValLeuGlyGlyProAspGlyThrLysValLeuLeuLysLysAlaGlySerVal 589
              ::: ||||||
Db   1561 TATATCTCCAAGAAGGGAGAGATATTGGGAAGGAGATGTACATCATCAACCAGAGGGCCAAGCTG 1620

Qy   590 PheGlyGlyIleSerSerLeuLeuAlaAlaGlyGly----------GlyAsnArgArgThrAla 606
              ::: |||
Db   1621 GCCGTGTG--GCTGATGAGTGGGGTCACCCAGTTCGTGGTCTCAGGGATGGCTGCAGCTAC 1677

Qy   607 AsnValAlaIleAlaHisGlyPheAlaAsnLeuLeuThrLeuLysSerThrLeuGlnGlu 626
              ::: ||||||
Db   1678 TTCGGGGGAGATCAGCATTCTGAACATCAAGGACGGGGAACCGGACGCCGGAGCGGC 1737

Qy   627 IleLeuValHisThrTyrProAspSerGluArgIleLeuGluMetLeuLysLysAlaArg---ValLeu 645
              ::: |||
Db   1738 AACATCCCAGCAATGGCTACCTCGTTCTGCCTCTCAAAGGACCATCTCATGGAG 1797

Qy   646 LeuLysGlnLys---------AlaLysThrAlaGlnIleAlaThrProProArgLysAspLeu 662
              ::: ||||||
Db   1798 GCCCTCACCGAGTACCCCGAGAAAGAGCCTGCGAGGAAGAAGGAACGGGACAGAGATCCTG 1857

Qy   663 AlaLeuLeuPheProProLysGluThrAsnProLysLeuProLysThrLeuLysLeuGly 682
              ::: ||||||
Db   1858 ATGAAAGACAACCTGATCGATGAGGAGGTGCCGAAGACGCGCCAAGGACACCTT 1917

Qy   683 ThrGlyLysSerAlaSerLeuLeuAlaArgLeuLeu--------------LysLeu 694
              ::: |::
Db   1954 ACCCTGCAGACCAGGTTTGCACGCGCCTCTGAGTGACGCCACCAGGACTGCTGAGGAAGATG 2013

Qy   695 LysArgGluGlnIleAlaLeuGlnLysSerGlyGlyGluGlu----- 711
              ||||| :::
Db   2014 AAGCAGCGTCTCAGCCAACTGGAAAGCCAGTTGGGAGGAGTGGGGAGCAAAGCCCCTGGCT 2073

Qy   712 GluGlyLysLysGluAsnGluAsnGluLysGlyGlnLys 728
              ::::::|||||
Db   2074 GATGGGGAGAGTTCCGGGGGGATGCTACAAAA---ACAGAGGACAAACACAG 2121

```
Qy    214  ThrAspArgLeuTyrLeuLeuLeuLeuValThrLeu------AlaTyrAsnTrp    231
                :::           |||||          ::|||||
Db    797  TCGGGAAACACATATTACACACTGGCCTGTTTTGCATCACATTACCTGTTATGTACAACTGG  856

Qy    232  AsnCysTrpPheIleProLeuArgLeuValPheProTyrGlnThrAlaAspAsnIleHis  251
                :::
Db    857  ACA------ATGGTTATTGCCAGAGACATGTTTGATGAACTTCAAATCTGATTACCTAGAA  910

Qy    252  TyrTrpLeuIleAlaAspIleIleIleCysSerAspTyrLeuTyrAspSerMetLeuPheIle  271
                ||||||           ::::|||||
Db    911  TATTGGCTCATTTTGGATTACGTTACGTCAGACACATAGTCTATTTAATCGATATG---TTTGTA  967

Qy    272  GlnProArgLeuGlnPheValArgGlyValGlyAspIleIleValAlaAspSerArgAsnGluLeuArg  291
                ::::           ||||||
Db    968  CGAACAAGGACAGGTTACCTACGAACAAGGACTGCTGGTTAAAGGAGAAGAACTTAAACTCATA  1027

Qy    292  LysHisTyrArgThrSerThrHisLysPheGlnLeuAspValAlaLeuSerIleLeuIleProProPheAsp  311
                :::           ||||||
Db   1028  AATAAATATAAAATCAACTTGCAAATTTAAACTTGATGTTCTGTCACTGATACCAACTGAT  1087

Qy    312  IleCysTyrLeuPhePheGlyPheAsn---ProMetPheAlaAsnArgMetLeuLys  330
                ||||||
Db   1088  TTGCTGTATTTTAAGTTAGGGTGGAACCTATCCAGAAAATTAGATTAAACAGAGTTTACG  1147

Qy    331  TyrThrSerPhePheGluProAsnHisHisLeuGlnSerIleIleMetAspLysAlaLysAlaTyrIle  350
                ||||||
Db   1148  TTCTTCTCCGTATGTGTTTGAGTTCTTCCAGAGAACAGAAAACTATACCAAACATC  1207

Qy    351  TyrArgValIleLeuArgThrArgGlyTyrLeuLeuPheIleLeuGluHisIleLeuAsnAlaCysVal  370
                ||||||           ::::
Db   1208  TTCAGGAATTTCAAACCTTGTTATGTATATGCGTCATCAATGGCATCTGAATGCATGTGTG  1267

Qy    371  TyrTyrTrpAlaSerAsnTyrGluGlyIleGlyThrThrArgTrpValTyr------  387
                ::::           :::
Db   1268  TTCTACTTCTATTTCTAAAGCTATTGGATTTGGAAATGATACAGGGTCTACCCTGATATT  1327

Qy    388  ---AspGlyGlu---GlyAsnGluTyrLeuArgCysSerTyrTyrIleProAlaVal  402
                |||           :::
Db   1328  AATGATCCTGAATTTGGCGGTTTGGCTAGAAAATACGTATACAGCCTTTACTCGGTCTACA  1387

Qy    403  ArgThrLeuIleThrIleGlyTyrLeuProGlnProGlnThrLeuProHisGluGlnIleLeuValPhe  422
                |||||||           ::|||||
Db   1388  CTGACTTTGACTACCATTGGTGAAACACCCCTCCGGTGGAGGGATTCTGAGTATGTCTTT  1447

Qy    423  GlnLeuLeuAsnPhePheSerGlyValPheValPheSerSerLeuIleGlyGlnIleMetArg  442
                ||           ::::
Db   1448  GTGGGTGGTTGATTTCCTAATTGGAGTGTTAATTTTGCTACCATCGTTGGTAACATAGGT  1507

Qy    443  AspValIleGlyValAlaAlaThrAlaAlaAsnGlnAsnTyrPheArgAlaCysMetAspAspThr  462
                |||           ::
Db   1508  TCTATGATTTCCAACATGAATGGCAGCAGAGAATTTCAAGCCAAGAATTGATGCTATC  1567

Qy    463  IleAlaTyrMetAsnAsnTyrSerIleProLysSerLeuValGlnLysSerArgValArgThrArg  482
                |||           ||||||
Db   1568  AAGCAAATAATGCATTTTCGAAATGTAAGCAAAGAGATATGGAAAAGAGGGTTATTAGAGTGG  1627

Qy    483  TyrGluTyrThrArgTrpAspSerGlnAsnArgMetLeuAspGluSerAspLeuLeuLysProThrLeu  502
                :::           ::|||
Db   1628  TTTGACTACCTGTGGCACCAACAAAAAAACAGTTGATGAGAAGAAGTCTTAAAGTATCTA  1687

Qy    503  ProThrThrValGlnLeuValAlaLeuAlaIleLeuAspValAsnPheSerIleLeuSerLysLysVal  522
                |||           ::::|||
Db   1688  CCTGATAAACTAAGAGCAGAAAATTGCCATCACGTTCACTAGACACATAAAAAAGGTA  1747

Qy    523  AspLeuPheLysLysGlyCysSerAspThrGlnMetIleTyrArgAspMetLeuLysLeuLysLysSer  542
                ||           :::
Db   1748  CGCATTTTTGCTGAATTGTGAAAGCTGGTGTCTTGTTGGTCTTGAAATTGCAACCC  1807

Qy    543  ValLeuuTyrLeuProGlyTyrAspPheValCysLysSerGlyIleLeuGlyLysGluMetTyr  562
                ||||           ::
Db   1808  CAAGTCTACAGTCCTGGAGATTATATTTGCAAGAAAGGGGATATCGGACGAGAGAATGTAC  1867

Qy    563  IleIleLysHisIleGlyGluValGlnValGlnLeuGlyGlyProAlaSerGlyThrArgLysValLeuLeuVal  582
                |||           :|:::
Db  27904  TTAGGTTTTCTCGAGCAAGGCTTAATGGTCAGTGAATACCAACAGCCTGTTGGCAGCGATTAC  27963
```

```
Alignment Scores:
Pred. No. :
Score:                    2.44e-71
                          748.50
Percent Similarity:       57.2%         Length:         32666
Best Local Similarity:    34.7%         Matches:        167
Query Match:              17.7%         Conservative:   108
DB:                                     Mismatches:     169
                                        Indels:         37
                                        Gaps:           11

US-09-855-828-1 (1-809) x US-09-949-016-16086 (1-32666)
```

```
Db   1868  ATTATCAAGGACAGGCAAACTCGCTGTGGTG---GCAGATGAGTGAGTCACTCAGTTGTG  1924

Qy    583  ThrLeuLysAlaGlySerValPheGlyGlyIleIleLeuSerLeuLeuUalAlaAlaGlyGly------  600
                |||           :::
Db   1925  GTATTGAGCGGATGGCGACTGCAGCTACTTCGGTCGAGGGAGATCAGCATTCTTAACATTAAAGGGAGCAA  1984

Qy    601  ---GlyAsnArgArgThrAlaAsnValAlaValAlaLAlaHisIleGlyPheAlaAsnLeuLeuThrLeu  619
                :::           ||||||
Db   1985  GCTGGCCAATCGAGAGAAACGGCCCAATATTAAAAGTATTGGCATTCAGAGACCTTGGTCGTCTC  2044

Qy    620  AspLysGlyLysThrLeuGlnLeuIleIleLeuGlnLysAla------LysThrAlaGlu  639
                ::::           ||||||
Db   2045  TCAAAAGATGAGACTTCACTGGAAGGCTCTACTGAGTCACCAAAAACTATCCTGGAA  2104

Qy    640  LysHisLysAlaArgValIleLeuLeuLysGlnLysAla------LysThrAlaGlu  655
                :::           ||||||
Db   2105  GAGAAAGGGAGCAGAGGATTTTAAGATGGGTCTCACTAGAGACCTTC  2164

Qy    656  ThrProProAlaArgLysAspLeuAlaLeuLeuPheProProLysGluGluThrProLysLeu  675
                ::::           ||
Db   2165  GGCAGTGATCCTAAAGACTCTTGAGAGAAGAGGGTTACTCAGGAGACACTTC  2224

Qy    676  PheLysThrLeuLeuGlyIleGlyThrGlyLysAlaSerLeuLeuArgLeuLeu------  692
                :::           ||
Db   2225  CTGCAAACC------AGGTTTGCCCAATCTTGGCGTGAGTAT  2260

Qy    693  ---------LysLeuLysArgGluGlnAlaLeuAlaGlnLeuLysLys---------  703
                |||           ::::
Db   2261  GAGTCCATGCAGCAGAGAAACTGAAAAACAAAGATTAACCAAGGTTGAGAAATTCTGAAACCG  2320

Qy    704  ------GluAsnSerGluGly---GlyGluGluGlyGlyGly  713
                ::           ||||||
Db   2321  CTTATTGACACAGAATTTTCAAGTATTGAGGGACCTGGAGCGCGGGAAAGTGG  2371
```

RESULT 6
US-09-949-016-17420
Sequence 17420, Application US/0994016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17420
LENGTH: 84571
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84571)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17420

Alignment Scores:
Pred. No.:   3.0e-64
Score: 692.00
Percent Similarity: 54.2%
Best Local Similarity: 33.8%
Query Match: 16.3%

Length: 84571
Matches: 160
Conservative: 97
Mismatches: 173
Indels: 44
Gaps: 10

US-09-855-828-1 (1-809) x US-09-949-016-17420 (1-84571)

Qy   275 LeuGlnPheValArgGlyGlyAspIleIleLeuValAspSerAsnGluLeuArgLysHisTyr 294
          ||| :::||||:::: :::|::
Db 80752 TTAGGTTACCTAGAACAACAAGGACTGCTGGTTAAAGGAAGAAGAACTTCATAAATAAATAT 80811

Qy   295 ArgThrSerThrLysPheGlnLeuAspValAlaSerIleIleLeuProPheAspIleCysTyr 314
          ||||||||||||||:: :||||||:::||||:|: :::|||:::||:|| :: :|
Db 80812 AAAATCCAACTTGCAATTTAAACTTGATGTTCGTCACTGATACCAACTGATTTGCTGTTAT 80871

Qy   315 LeuPhePheGlyPheAsn---ProMetPheArgAlaAsnArgMetLeuLysTyrThrSer 333
          |||| ||||||||:::|| |||:|| :||:||||:::||||:::|||||:: :||:
Db 80812 AAAATCCAACTTGCAATTTAAACTTGATGTTCGTCACTGATACCAACTGATTTGCTGTTAT 80871

Qy   295 ArgThrSerThrLysPheGlnLeuAspValAlaSerIleIleLeuProPheAspIleCysTyr 314
Db 29040 ...
Qy   315 LeuPhePheGlyPheAsn---ProMetPheArgAlaAsnArgMetLeuLysTyrThrSer 333
Qy   334 PhePheGluPheAsnHisHisLeuGluSerIleMetAspLysAlaTyrIleTyrArgVal 353
Qy   354 IleArgThrThrGlyTyrLeuPheIleLeuHisIleHisAsnAlaCysValTyrTyrTrp 373
Qy   374 AlaSerAsnTyrGlyGlyIleGlyThrThrArgTrpValTyrAspGly 389
Qy   390 GluGlyAsnGluTyrLeuArgCysTyrTyrTrpAlaValArgThrLeu 405
Qy   406 IleThrIleGlyTyrLeuProGluProGlnThrLeuProPheGlnLeuLeu 425
Qy   426 AsnPhePheSerGlyValPheValPheSerSerLeuIleGlyIleMetArgAspValIle 445
Qy   446 GlyAlaAlaThrAlaAsnGlnAsnTyrPheArgGlyAlaCysMetAspAspThrIleAlaTyr 465
Qy   466 MetAsnAsnTyrSerIleProLysLeuValGlnHisLysArgValArgThrArgTyrGluTyr 485
Qy   486 ThrTrpAspSerGlnArgMetLeuAspGluSerAspLeuGluLeuSerThrLeuProThrThr 505
Qy   506 ValGlnIleuLeuAlaLeuValAsnPheSerIleIleSerLeuLysSerValAspLeuPhe 525
Qy   526 LysGlyCysAspThrGlnMetIleTyrAspMetLeuLeuLeuArgLeuLysSerValLeuTyr 545
Qy   546 LeuProGlyAspPheValCysLysLysGlyLysGlyLeuGlyValGluMetTyrIleLeuLys 565
Qy   586 AlaGlySerValPheGluValGlyIleLeuSerLeuLeuAlaLeuAlaGlyGly---GlyAsn 602
Qy   566 HisGlyGluValGlnLeuValLeuGlyValGlyTyrProAspGlyThrLeuValThrLeuLys 585
Qy   603 ArgGlyThrArgAlaAsnValAlaIleAlaHisGlyPheAlaAsnLeuLeuThrLeuAspLys 622
Qy   623 ThrLeuGlnGlnIleLeuLeuValHisTyrProAspSerGluArgIleLeuLeuMetLysLys 642
Qy   643 Arg---ValLeuLeuLysGlnLys--------AlaLysThrAlaLeuGluAlaThrProPro 658
Qy   659 ArgLysAspLeuAlaLeuLeuPheProProLysGluGluThrProLysGluPheLysThr 678
Qy   679 LeuLeuGlyGlyGlyThrGlyLysLysAlaSerLeuAlaArgLeuLeu 692
Qy   693 LysLeuLysArgGluGluGlnHisLeuAlaLeuAlaGlyHisLysLysGluAsnSerGluGlyGlu 710
Qy   711 Glu---------GlyGlyLysGluAsnGluLysLysGluAsnLysGluAsnLysLysGln 727
Qy   728 Lys 728
Db 29316 CAG 29314

RESULT 7
US-09-927-267-2
; Sequence 2, Application US/09927267
; Patent No. 6933147
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: iCAgen, Inc.
; TITLE OF INVENTION: CNG2B; A No. 6933147e1 Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 018512-0065100US
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2308
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)
; OTHER INFORMATION: complete nucleotide sequence derived from assembly
; OTHER INFORMATION: of PCR fragments
; NAME/KEY: CDS
; LOCATION: (333)..(2060)
; OTHER INFORMATION: CNG2B
US-09-927-267-2

Alignment Scores:
Pred. No.:
Score: 1.85e-64
Length: 2308
Percent Similarity: 46.3%   Matches: 202
Best Local Similarity: 27.3%   Conservative: 140
Query Match: 15.8%   Mismatches: 295
DB: 3   Indels: 103
                                      Gaps: 25

US-09-855-828-1 (1-809) x US-09-927-267-2 (1-2308)

```
Qy    178  AspLysProThrGluHisThrTyrTyrArgLeuLeuTrpPheTyrLysValLysMetProLeu 197
                |||||          |:::
Db    417  -------------------CCATCTGGGGATTACTAC---------TACTGG------------ 440

Qy    198  ThrGluTyrLeuLysArgIleLysLeuProAsnSerTyrThrArgArgLeu 217
                |||
Db    440                                                     440

Qy    218  TyrLeuLeuTrpLeuLeuLeuValThrLeuAlaTyrAsnArgCysThrPheIlePro 237
                ||:
Db    441  ------------TGGCTGAACACAATGGTCTTCCCAGTCGATATAACCTCATCCTCGTG 440

Qy    238  LeuArgLeuValPheProTyrGlnThrAlaAspAsnIleHisTyrTrpIleAlaAsp 257
                |||||                |||
Db    492  TGCAGAGCCGCTGCTCCCCGACTTGCAGCACGGTTATCTGCAGCACTGTGCTGGAC 491

Qy    258  IleIleCysAspIleIleTyrLeuTyrAspMetLeuPheIleGlnProArgLeuGlnPhe 277
                 :::::||||||||                     :||:
Db    552  TACACGAGTGACCTGCTATACCTACTAGACATGTG--GTGCGCTTCCACACAGGATTC 551

Qy    278  ValArgGlyGlyAspIleIleValAlaAspSerAsnGluLeuArgLysHisTyrArgThrSer 297
                     |||                       :::
Db    609  TTGGAACAGGGCATCCTGGTGGTGGCAGACTCGAAGGAGCTCAGGAAGCACTATCGGTCAC 608

Qy    298  ThrLysPheGlnLeuAspValAlaAlaSerIleIleIleProPheAspAspIleCysTyrLeuPhePhe 317
                 |||||              ||||:|               :::
Db    669  TGGGAGTTTCTTCTTGGAACTGGACCTGCTATCCCTATACTTTCGGCGGCTG 668

Qy    318  Gly------PheAsnProMetPheAspArgAlaAsnArgMetLeuLeuTyrThrSerPhePheGlu 336
                   |||                                :::
Db    729  GGCCCGCACACACCCCTGAGCGTGACCGGCTTTCTCCCGGACCTGGCCCTTCGAG 728

Qy    337  PheAsnHisHisLeuGluSerIleMetAspLysAlaTyrIleTyrArgValIleArgThr 356
                 |||||                            :||:
Db    789  GCCTTCGACCGACAGCAGACCCGGAACTCTACCCAAATGCCTTTCGCATTGCCAAGCTG 788

Qy    357  ThrGlyTyrLeuLeuPheIleLeuAsnAlaCysSerValTyrTyrTyrArgAlaSerAsn 376
                 |||||||                           :::
Db    849  ATGGCTTACATTTTTGTCGGTACATTCCATTGGACAGCTGCCTATACTTTGCCCTATCCCGG 848

Qy    377  TyrGluGlyIleGlyThrThrArgTrpValTyrArgAspGlyGluGly- 391
                   |||:||                        ||:
Db    909  TACTTGGGCTTCGGGGGTGTGACGCAGGTGTACCCGGACAGCCTGGCTTTGAG 908

Qy    392  ------------AsnGluTyrLeuArgCysTyrTyrTyrAlaValArgThrLeuIleThrIle 408
                     ::||||||                       |||
Db    969  CGGCCTGCGGCGGCCCAGAGACCCTAATAGCTTTTACTTCCCGATACTGACTACAGTG 968

Qy    409  GlyGlyLeuProGlnProGlnThrLeuPheGluIleValPheGlnLeuLeuAsnPhePhe 428
                 ||||||                          :||
Db   1029  GGCGGATACACCGCCGCCAGCCAGGGAAGAGAGTACCCTCTTCATTGGTGGCGACTTCCTG 1028

Qy    429  SerGlyValPheValPheSerSerLeuIleGlyThrLeuGlnMetArgAspValIle--GlyAla 447
                   |||                                   |||
Db   1089  CTGGCCGTCATGGGGTTTGGCCACCATCAAGGGTAGCATGAGCTCTGCATCTCAACAACATG 1088

Qy    448  AlaThrLeuAlaAsnGlnAsnTyrPheArgAlaCysMetAspAspThrIleAla--------Tyr 465
                   :::||||||                                |||
Db   1149  AACACTGCGAGATGCGGCTTTCTAC----------------CCAGATCATGCACTCGGTGAAGAAGTAC 1148

Qy    466  MetAsnAsnTyrSerIleProLysSerLeuValGlnLysArgThrArgThrTyrGluTyr 485
                 ||||||
Db   1200  ATGAAGCTGCAGCACAGTCAACCGCAAGCTGGAGCCGCGGAGTTATTGACTGGTATCAGCAC 1199

Qy    486  ThrArgTrpAspSerGlnArgMetLeuGluAspLeuLeuLysThrLeuProThrThr 505
                 |||                                 :::
Db   1260  CTGCAGATCAACAAGAAGATGACCAACGAGGTGACCACCATTACAGCACTTGCTCGAGCGG 1259

Qy    506  ValGlnLeuLeuAlaIleLeuAspProValAlaAsnPheLeuPhe 525
                 |||           :::
Db   1320  CTGGGGGGCGAAGCGGGCCTGTGTCTCCACTCGTGCGGGGTTGCAGGAATCTTT 1379

Qy    526  LysGlyGlyCysAspThrGlnMetIleTyrArgAspMetLeuLeuLeuArgLeuLysSerValLeuTyr 545
                :::
Db   1380  CAGAACTGTGAGGCCGCAGCCTGCTTGGAGGAGGACGTGGGTGGGTGCTGGAGCTGGAAGCTGCCCCCAGACCTAC 1439

Qy    546  LeuProGlyAspPheValCysLysSerGlyIleGlyIleGluGlyLysGlyGlyMetTyrIleIleLeuLys 565
                 |||
Db   1440  TCACCAGGTGAATATCTTATGCGCGAAAGGGAGGACTTGGGCACATTGCATCTTTTTTGACTTGCACA 1499

Qy    566  HisGlyIleGlyValGlnValLeuGlnGlyGlyGlyProAspGlyProGlnAsn 585
                 |||                            :::
Db   1500  GAGGGTCAACTGGGCGTGGTG--GCAGAGATGAGTGTATCACACGTGACTCCGGT 1499

Qy    586  AlaGlySerValPheGlyIleLeuSerLeuLeuAlaLysGly-------- 602
                 |||                             :::
Db   1557  GCAGGGCCTTACTTGGCCACAGTCAAGCAGACTCAGACTGGAACATGTCTGGGAAC 1616

Qy    603  ArgArgThrAlaAsnValAlaAlaHisGlyPheAlaAsnLeuLeuThrLeuAspLysLys 622
                 |||                             :::
Db   1617  CGCCCCGACCACGGCCAACATCAAGAGACCCTAGGTTATTCAGACCTTATTCTGCCTGAGGAG 1616

Qy    623  ThrLeuGlnGluIleLeuLeuValHisTyrProAspSerGluArgIleLeuLeuMetLeuLysSerAla 642
                 |||
Db   1677  GACCTGCGGGGGACGGTTGCTGACGGAGTATCCAGACAGACCATCATGGAGGAGAAGGA 1736

Qy    643  Arg-----------ValLeuLeuLys------------------------GlnLysAlaThrAla 653
                |||
Db   1737  CGTGAGAACTCTGCTGAAAAATGAACAAGTGGACGTGAAATGCCCAGCTGAGACTGCC 1796

Qy    654  ------GluAlaThrThrProProAlaArgLysAspLeuAlaLeuPheProLysGluGlu 671
                   |||                                     :::
Db   1797  CTGCACAGGAGCCCACAGAGTCCCG------CTACGAGGCCTTAGACCAGCACTGGATGAT 1796

Qy    672  ThrProLeuSerPheLysThrLeuLeuGlyLysGlyAlaSerLeuLeuAlaArgLeu 691
                 :::||||||
Db   1851  CTACAGACACCAAGTTTGCTCGCCTCCTGGGTGGAGTGGCCACTTAAGAATTGCT 1910

Qy    692  LeuLysLeuLysArgGlyGluCysThrAlaSerProIleAlaValAlaGluGluGlu 707
                 |||                                :::
Db   1911  TACCGGCCATTGAACGGCTGGGAGTGGCCAAAGTGCCCAGCTGGAGAGAGACTGGGCT 1970

Qy    708  GlyGlyGlyValGluGlyLysLysGluAsnGlyGluGlyGlnLysGluGlyGln 727
                 |||                                ::
Db   1971  GAGGGCTGATGAGGGCCACGAGGGGAGCCCTGAGGAGGAACTTCCAAAGATGAAGAG 2021

Qy    728  LysGluAsnGluAspLysLysGlyLysAsnGluAspProLysLysGlyArgGlu---------Pro 746
                 |||                                :::
Db   2022  ------------------GGCAGGGGCCCAGCCCAGGGCCAGGTTGCAGCAGAGTGACCC 2063

Qy    747  GluGluLysProLeuAspArgProCysThrAlaSerProIleAlaValGluGluGlu 766
                 |||
Db   2064  CATCCCCATACCCCAGGAATTC--CCACCTCCTAGTGAATCCAGAGTGTGTAGTA--AAG 2116

Qy    767  ProHisSerSerValArgArgThrValLeuProArgGlyThrSerArgGlnSerLeuIle 785
                 :::
Db   2117  CCTAACTGCTTCCAACTCTGTCATCCTCGTTCTGCGAGATCACAGACAGGACGGAATT 2173
```

RESULT 8

US-09-799-451-351

; Sequence 351, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei

APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 67839969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_Fl_genes Version 2.0

; SEQ ID NO 351
; LENGTH: 2366
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (639)..(2363)
US-09-799-451-351
Query Match: 15.8%

Alignment Scores:
Pred. No.:
Score: 669.00
Percent Similarity: 46.8%
Percent Identity: 27.4%
Best Local Similarity: 15.8%

US-09-855-828-1 (1-809) x US-09-799-451-351 (1-2366)

Length: 2366
Matches: 191
Conservative: 135
Mismatches: 276
Indels: 94
Gaps: 23

2.2e-64

Qy   73 LeuSerLysLysAsnSerSerGlyAspLeuThrThrAsnProGlnAsnAlaAla   92
          ::|:||| ||||||||||||::|||
Db   462 ATCAGTAGTAGCCGCTAGCTTCTGGTTGTTGTTGTTAAGAGCCCAAAGACAAAGAAGAGTC--- 518

Qy   93 GluProThrGlyThrValProGlnGlnLysGluMetAspProGlyLysGluGly------ 110
          |||
Db   519 --------ACAGCAGAAGCCCACACAGCACCCTCCTTCAGGCAGGTCAGGCACTAGTG----- 566

Qy   111 ProAsnSerProGlnAsnLysProProAlaAlaProValIleAsnGluThrTyrAlaAspAla 130
          ||||||||
Db   567 CCCAACTCC--AGAAGTCCCCTACAGCAGCAGAGAGGTGTTGGAACATCTCACACCCCAGCA 623

Qy   131 GlnLeuHisAsnLeuValLysArgMetArgGlnThrAlaLeuTyrLysLysLysLeu 150
          ||:
Db   624 CCAGACCAC--AGAACCATGAGCCAGGACACC--AAAGTGAAGACA 665

Qy   151 ValGlyGlyAspLeuSerSerProGlnThrAlaLysProThrAlaVal 170
          ||||
Db   666 ACAGAG------TCCAGTCCC--CCAGCCCATCCAAGCCACAGAAGTTG 707

Qy   171 ProProValLysGluSerAspAspLysProThrGlyHisThrTyrArgGlnLeuLeuTrpPhe 190
          :::
Db   708 CTGCCCGTCCCCGGAC------CCATCTGGGGAGGATTACTAC-- 746

Qy   191 LysValLysLysMetProLeuThrGluTyrLeuLysArgIleLysLysLeuProAsnSerIle 210
          |||
Db   746 746

Qy   211 AspSerTyrThrAspArgGluTyrLeuLeuTrpLeuLeuValThrLeuAlaLeuTyrAsn 230
          :::
Db   747 TGGCTGAACACAGATGGTCTTCCCAGTCATG 776

Qy   231 TrpAsnCysTrpPheIleProLeuArgLeuValPheProTyrGlnThrProAlaAspAsnIle 250
          |||
Db   777 TATAACCTCATCATCTCGTGTGTGCAGAGCCTCGTTCGACTTGCCACGGTTACTG 836

Qy   251 HisTyrTrpLeuIleAlaAspIleIleIleCysArgAspIleIleIleTyrLeuTyrAspMetLeuPhe 270
          |:|:||| |||||||||||||||::|
Db   837 GTGGCCTGGGTTGGTGCTGGAGCTACACGAGTGACCTGCTCTATACCTACTTAGTGGTG--- 893

Qy   271 IleGlnProArgLeuGlnPheValArgGlyGlyAspIleIleValAspSerAsnGluLeu 290
          ::::
Db   616

RESULT 9
US-09-927-267-3

; Sequence 3, Application US/09927267
; Patent No. 6933147
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: CNG2B: A No. 6933147el Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 01512-00651US
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)
; OTHER INFORMATION: coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(1728)
; OTHER INFORMATION: CNG2B

US-09-927-267-3

Alignment Scores:
Pred. No.:
Score: 4.79e-63
Percent Similarity: 655.00
Best Local Similarity: 50.6%
Query Match: 29.2%
DB: 15.5%

US-09-855-828-1 (1-809) × US-09-927-267-3 (1-1728)

Length: 1728
Matches: 165
Conservative: 121
Mismatches: 241
Indels: 38
Gaps: 14

Left column

```
RESULT 10
US-09-949-016-38930/c
; Sequence 38930, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38930
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-38930

Alignment Scores:
  Pred. No.:
  Score:                  3.81e-53
  Percent Similarity:     560.00
  Best Local Similarity:  100.0%
  Query Match:            13.2%
  DB:

          Length:       601
          Matches:      109
          Conservative:   0
          Mismatches:     0
          Indels:         0
          Gaps:           0

US-09-855-828-1 (1-809) x US-09-949-016-38930 (1-601)
```

```
Qy   1237 TTTGGGGAGATCAGCATCATCAACACATCAAAAGGGAACAATGTCTGGGAACCGCGCACAGCC 1296
Db   1237 |||                                                          ||| 1296
Qy    607 AsnValValAlaAlaHisGlyPheAlaAsnLeuLeuThrLeuAspLysLysThrLeuGlnGlu 626
Db   1297 AACATCAAGAGCCTAGGTTATTCAGACTTATCTGCCTGAGCAAGGAGGAACCTGCGGAG     1356
Qy    627 IleLeuValHisTyrProAspSerGluArgIleLeuMetLysLysLysAlaArg---Valleu 645
Db   1357 GTGCTGAGCGAGTATCCACACAGCAGACCAATCATGGAGGAGAAGAGGACGTGAAGGATCCTG 1416
Qy    646 LeuLys-------------------------GlnLysAlaLysThrAla----GluAla     655
Db   1417 CTGAAAAATGAACAAGTTGGACCTGAGGCAGCAGGCAGCTGAGATCGCCCCTGCAGGAGGCC  1476
Qy    656 ThrProProArgLysAspLeuAlaLeuLeuPheProProLysGluThrProLysLeu       675
Db   1477 ACAGAGTTCCCG---------CTACGAGGGCCTAGACCAGCAGCTGGATGATCTACAGACCAAG 1530
Qy    676 PheLysThrLeuLeuGlyGlyThrGlyGlyLysAlaSerLeuAlaArgLeuLeuLysSerLeu  695
Db   1531 TTTGCTCGCCTCCTTGGCTGAGCTGAGGTCCAGCGACTTAAGATTGCTTACCGCATTGAA    1590
Qy    696 ArgGluGlnAlaAlaAlaGlnLysLys-------------GluAsnSerGluGlyGlyGlu    711
Db   1591 CGGCTGGAGTGGCAGAGTGGCCAATGCCCCGAGGACCTGGCTGCTGAGGCTGATGAC        1650
Qy    712 GluGlyLysGluAsnGluAspLysLysGlnLysGlyGluAsnGluGluAsnGlu          731
Db   1651 GAGGGTGAGCCTGAGCAGGAGGAACTTCCAAAGATGAAGAAGAGGGCCAGCCAGGAGGA     1710
Qy    732 AspLysGlyLysGlu  736
Db   1711 CCCCAGGTCCAGAG  1725
```

```
US-09-855-828-1 (1-809) x US-09-949-016-38930 (1-601)
Qy    701 GlnLysGlyLysGluGluAsnSerGluGluGlyGluGlyLysGluAsnGluAspLysLysGln  720
Db    234 ATTGCAGTGGAGAAGGAAGAGGCAGTTTTACCGGAGGAGGA                        175
Qy    414 CAGAAGAAAGAAAATTCTGAAGGAGGAGGAGGAGGAGAAAGAGGAAGAAAATGAAGATAAAACA 355
```

Right column

```
RESULT 11
US-09-949-016-205286/c
; Sequence 205286, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205286
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-205286

Alignment Scores:
  Pred. No.:
  Score:                  3.81e-53
  Percent Similarity:     560.00
  Best Local Similarity:  100.0%
  Query Match:            13.2%
  DB:
          Length:       601
          Matches:      109
          Conservative:   0
          Mismatches:     0
          Indels:         0
          Gaps:           0

US-09-855-828-1 (1-809) x US-09-949-016-205286 (1-601)
```

```
Qy    721 LysGluAsnGluAspLysLysGlyLysGluAsnGluAspLysLysGlyLysGluAsnGluAspLys 740
Db    354 AAAGAAAATGAGGATAAACAAAAAGGAAAAGAAAATGARGATAAA                       295
Db    414 CAGAAGAAAGAAAATTCTGAAGGAGGAGGAGGAGGAGAAAGAGGAAGAAAATGAAGATAAAACA   355
Qy    741 AspLysLysGlyArgGluProGluGluLysSerProLeuAspArgProGluCysThrAlaSerPro 760
Db    294 GATAAAGGAAGAGCCAGAAGAGAAGCCAGACAGATGCAGGAAGCCACTGGACACAGAGTGTACAGCAGAAGTCCT 235
Qy    761 AspLysLysGlyArgGluProGluLeuGluSerProArgProGluCysThrAlaSerPro     780
Db    234 ATTGCAGTGGAGAAGGAAGAACCCACTCAGTTAGAAGGAGGACAGTTTTACCGGAGGAGGA   175
Qy    761 IleAlaValAlaGluGluLeuGluHisSerValArgGlyThrValLeuProGluArgGlyThrSer 780
Db    781 ArgGlnSerLeuIleIleSerMetAlaProSerAlaGluGluGluGluValGluHisGlnArgGln 800
Qy    781 ArgGlnSerLeuIleIleSerMetAlaProSerAlaGluGluGluGluValGluHisGlnGln   800
Db    174 CGTCAATCACTCATTATCAGCATGGCTCCTTCTCTGCCTGAGGGCGGGGAAGAAGAAGTCTCTACT 115
Qy    801 IleGluValLysGluLysAlaLysGln 809
Db    114 ATTGAAGTCAAAGAAAAGGCTAAGCAA 88
```

```
Db   174  CGTCAATCACTCATTATCAGCATGGCTCCTTCTGCCTGAGGCGGGAGAGAGGTTCTTACT  115
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   801  IleGluValLysGluLysGlnSer  809
Db   114  ATTGAAGTCAAAAGAAAAAGGCTAAGCCA  88

RESULT 12
US-09-949-016-12816
; Sequence 12816, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE:  2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE:  2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE:  2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE:  2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12816
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12816

Alignment Scores:
Pred. No.:
Score:                  3.05e-49
Percent Similarity:     60.00
Best Local Similarity:  18.7%
Query Match:            18.6%
DB:                     13.2%

                        Length:          99370
                        Matches:         215
                        Conservative:    1
                        Mismatches:      5
                        Indels:          936
                        Gaps:            2

US-09-855-828-1 (1-809) x US-09-949-016-12816 (1-99370)

Qy   589  ValPheGlyGluIleSerLeuLeuValAlaGlyGlyGlyAsnArgArgThrAlaAsnVal  608
             ::::||              ||     ||
Db  93846  ATTTTTCTCTTACAGCCTTCTAGCACGCAGGAGGAAACCGTCGAACTGCCAAGTG  93905

Qy   609  ValAlaHisGlyPheAlaAsnLeuThrLeuAspLysThrLeuGlnIleIleLeu  628
             |||||||||||
Db  93906  GTGGCCCACGGGTTTGCCAATCTTTTAACTCTAGACAAAAAGACCCTCCAAGAAATTCTA  93965

Qy   629  ValHisTyrProAspSerGluArgIleLeuMetLysLysLysAla  642
             ||||||||||
Db  93966  GTGCATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAAGC-CAGGTACAAACTTTAAAA  94024

Qy   642                                                    ArgValLeuLeuLys  647
Db  94025  CACCATTAGAGAGATGGAGTGGGTTTTACTTTGTAAACTCTGAGATAGGGAGAACCCT  94084

Qy   642  ----------------------------------------------------------  642
Db  94085  ATTATGATTGTGATAAACTGATCACAGTGAGATATGCTTAATGAACAACTATTAATGTA  94144

Qy   642  ----------------------------------------------------------  642
Db  94145  GGTACCCATTGAAAACTACACAGTTAGGATAAAATTGCAGTTTTTTTTAGTAGATTTTGCCA  94204

Qy   643                                               ArgValLeuLeuLys  647
Db  94205  GAACTCTCACAGAGTTACCTAAAACAGCTTTTCTTCCTTACCCACAGAGTGCTTTTAAAG  94264

Qy   648  GlnLysAlaLysThrArgLeuAlaThrProArgLysAspLeuAlaLeuLeuPhePro  667
             ||||||||||||||
Db  94265  CAGAAGGGCTTAAGACCGCAGAAGCAACCCCTCCAAGAAAAAGATCTTGCCCTCTTCCCA  94324
```

```
Qy   668  ProLysGluGluThrProLysLysLeuPheLysThrLeuLeuGlyThrGlyLysAlaSer  687
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  94325  CCGAAAGAAGAGACACCAAAGAAACTGTTTAAAACTCTCCTAGGGAGGGCACAGGAAAAGCAAGT  94384

Qy   688  LeuAlaArgLeuLeuLysLysArgGluGlnAlaAla  700
             ||||||||||||||||||||||||||||
Db  94385  CTTGCAAGACTACTCAAATTGAAGGAGGAGCAGC-TCAGGTAATAAGGTGGAGTGA  94443

Qy   700  ----------------------------------------------------------  700
Db  94444  ATGGACGGGCTGTCATGGGAGGAGGCCCCAGACTAAGTATATACACAACAAAGCGCCACTCTA  94503

Qy   700  ----------------------------------------------------------  700
Db  94504  ATTCCATTTCAGACACTGGGAATGATTTGGGACTAATCTAATACTAATACTCCTGCTTTAT  94563

Qy   700  ----------------------------------------------------------  700
Db  94564  ATATAGCACATTATTATTTAAACTGCTGAATTCCACATATCATCACATTTAAACCCTCAC  94623

Qy   700  ----------------------------------------------------------  700
Db  94624  AGGATGTTTATTAGATGGGCTTTAAATATGCATTGTAATTTATAAAACAGAGTATACCCTCATTAT  94683

Qy   700  ----------------------------------------------------------  700
Db  94684  TCATAGATTATTTGCAGATTCTATATTGGTGAATCTACTTACTATAATTATTAGTAACT  94743

Qy   700  ----------------------------------------------------------  700
Db  94744  TAAAATCAATACTACTACTGGTGCTTTTGTGGTCATTGTTGTGGACAACAGCACCTGCAGGGTGG  94803

Qy   700  ----------------------------------------------------------  700
Db  94804  CAAAAAAATTTAAGTTGCTTGAATGCATACATTTCAGCTGAGTTTGAAAAAAGAGGCACTC  94863

Qy   700  ----------------------------------------------------------  700
Db  94864  TCCTTTCTTGTTTCAGCTCTGATACTATAAACGAATGACCCTTGGCCGGGGTGCGGGTGGCT  94923

Qy   700  ----------------------------------------------------------  700
Db  94924  CACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGGCAGGAGAT  94983

Qy   700  ----------------------------------------------------------  700
Db  94984  CGAGACCATTCTGACTAACACGGTGAAACCCTGTCTCTACTGAAAACACAAAAAATTAGC  95043

Qy   700  ----------------------------------------------------------  700
Db  95044  CGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAAGAGAATTG  95103

Qy   700  ----------------------------------------------------------  700
Db  95104  CTTGAATCCGGGAGGCGGAGGTTGTTAGTGAGCCGAGATCACACAACACTGCACTCCAGCCTG  95163

Qy   700  ----------------------------------------------------------  700
Db  95164  GGCGACAGAGCGAATACTCTGTCTCAAAAAACAAAACAAAAACAAAACAACAACAAAAA  95223

Qy   700  ----------------------------------------------------------  700
Db  95224  AGAGTGACACTTTAGTGCCATGCTTTCCACATTTTTGTGCTTTTGCATGTGTGTGATT  95283

Qy   700  ----------------------------------------------------------  700
Db  95284  TTGCTGCTTAAAAATAGCCCCAAGCATAGTCCTGAAATACTGTCTTAGTGTGCTTCCTAAGTGC  95343

Qy   700  ----------------------------------------------------------  700
Db  95344  CAAAAATGCTCGTGATGTGCCTTCCAGAGAAAATATGTGTGTTAGGTGAAACTTCATTCAGGC  95403
```

```
Db  95404  ATTACAGTGCTGTTTGCATGAGTTCAATATAATGAATCAATAATACCTCAAATTAATCAA  95463
Qy    700  ------------------------------------------------------------    700

Db  95464  TTGATCAAAATTAAATAGTGTATCTCTAAACAAAAACACACATGAAACAAAGTTATACATT  95523
Qy    700  ------------------------------------------------------------    700

Db  95524  GACCAATTGACAAAAATATTATGGCTTGAACCATAATATCTCATAGGAATAGTTAAAATAT  95583
Qy    700  ------------------------------------------------------------    700

Db  95584  ATTTCCTCCAAGAACAATGGGTTCAGTACTTGCTCGTGTTTGTGTGGAAAAATTTATAG   95643
Qy    700  ------------------------------------------------------------    700

Db  95644  AACAAAACTACATGAATAAAAATCAACTGTATATATACAGACATACATATGGATATATAA   95703
Qy    700  ------------------------------------------------------------    700

Db  95704  ATAAATAACCATTTTATCAACATTTTCACAAATATTACTATATAGATCACAAATGT      95763
Qy    700  ------------------------------------------------------------    700

Db  95764  TTAAAGCCCAAAATAACTTTGTAAATTTCATCCAAGCTTTTCATGTTATATAGATGAGAAA  95823
Qy    700  ------------------------------------------------------------    700

Db  95824  CTGAAAAACCAGATCAAGGGATTTGGATAAGATCATAATTAGTTACAGAGCAGAAAGCTAT  95883
Qy    700  ------------------------------------------------------------    700

Db  95884  TACTCAGGTGTTCAGACTTACAGGCCTACACTAAGCTCCCTTTCAATTCCTAAAAATGTA   95943
Qy    700  ------------------------------------------------------------    700

Db  95944  AAGAAAACTCAAATGTTATTGTTTCTCTCTCTCTTTTTTTTGGTTTCATATTTC        96003
Qy    700  ------------------------------------------------------------    700

Db  96004  TTTGATTCTCATAATTAGCCTATGAGGGGCAGATATTGAGAAACAGAGAGAGCAGGGGATTC  96063
Qy    700  ------------------------------------------------------------    700

Db  96064  AGGTTTTCTGAACCTAGTCATTATGTTATCTCTAAAACTGTAGAAATGGGTAGCTGTGGA   96123
Qy    700  ------------------------------------------------------------    700

Db  96124  CCTTTCAGAAAATAAGTAAAGCACATATTATAAAGTCAGTCACTACAAAAAGATGAAAAC   96183
Qy    700  ------------------------------------------------------------    700

Db  96184  TTGCATTTTCCTTTTCCACACATCAACACTGTGGGTGAAAAGTTAGGGATCCAGTATAAAC  96243
Qy    700  ------------------------------------------------------------    700

Db  96244  CAAATGCTTCATTTGCATCAGCATAGAAATAATTAATTTGCATAAAAAAGTTATGGGGAGTA  96303
Qy    700  ------------------------------------------------------------    700

Db  96304  AAGAAATATATAAGTAAAAATGTGTTAAGAATCTCAACTTTATCTGTGCACATTCATATGTC  96363
Qy    700  ------------------------------------------------------------    700

Db  96364  AGGCAGAGCCTTTCTCAAATTGATCCCAAGCATTACCAGTGTAAAGAGCAATAGTGTTACCTTTT  96423
Qy    700  ------------------------------------------------------------    700

Db  96424  GCTATGAAATTTCTATAGCTAGTAGTGCTAAACACGATAGGTACAAAACATGACAGGTCAAGCA  96483
Qy    700  ------------------------------------------------------------    700

Db  96484  CCTGTGGGACAAATGGGAAAAGATCATACTAGGAAAAGGGATAAGTTCTCCCCTGAGGTTCT  96543
Qy    700  ------------------------------------------------------------    700

Db  96544  CCCACAAGCTTAGGCAGAGGAGAAAACCCTACTTTTTACAGTATTTTTATATAGTATTCGGT  96603
Qy    700  ------------------------------------------------------------    700

Db  96604  TAATATGTTTTTATTAAAAATAAAATATTTTATCTCTACAGAAATAAGTAAAAATAT      96663
Qy    700  ------------------------------------------------------------    700

Db  96664  TTAAAAGCAAAAACAGAGTCCTGAGCACTGAGTCTAATAATTCAGAGAGTATAAGGACC   96723
Qy    700  ------------------------------------------------------------    700

Db  96724  AATAGGAAGAGAATTCCTTGGCAGAGGACAAAAAATGCAATTCAGACTAACATCATGACT  96783
Qy    700  ------------------------------------------------------------    700

Db  96784  CAAAGGCAACACAGTCCATTCTCTAGCACACCAGAAACTTCGTCAAATGATAGTCAGAAGC  96843
Qy    700  ------------------------------------------------------------    700

Db  96844  AAAGCAGACATGATTCCTGGATTCACTTAATTCAGACAGTCTGTCTTGGTTGGATCTTA    96903
Qy    700  ------------------------------------------------------------    700

Db  96904  GCCATTGCATGCTAATCAAAATCTAATCCAAATCGTTTTTAATTACGATTTCAACACCAGTT  96963
Qy    701  ----------GlnLysLysGluAsnSerGluGluGlyGlyGlyLys                 714

Db  96964  CTTTGTAATTGTCCTTCCAGAGAGAAAATTCTGAAGGAGGAGGAGGAGGAGAAGAAGGAA    97023
Qy    715  GluAsnGluAspLysGlnLysGluAsnSerGluGluGlyGlyGly                  734

Db  97024  GAAAATGAAGATAAACAAAAAGAGAATAGTGAAGAAGGAGGAGGAGGA               97083
Qy    735  LysGluAsnGluAspLysGlnLysGluAsnSerGluGluGlyGlyGly               754

Db  97084  AAAGAAAATGAAGATAAACAAAAAGAGAATAGTGAAGAAGGAGGAGGAGGA            97143
Qy    755  GluCysThrAlaSerProIleAlaValGlnGluGluProHisSerValArgArgThrVal   774

Db  97144  GAATGTACAGCAAGTCCTATTGCAGTGCAGGAAGAACCCCACTCAGTTAGGAGGACAGTT   97203
Qy    775  LeuProArgGlyThrSerArgGlnSerLeuIleIleSerMetAlaProSerAlaGluGly   794

Db  97204  TTACCCAGGGGACTTCGTCAATCACTCATTATCACTGGCTCCTTCTGCTGAGGGC        97263
Qy    795  GlyGluGluValLeuThrIleGluValLysGluLysGlyAlaLysGln               809

Db  97264  GGAGAAGAGGTTCTTACTATTGAAGTCAAAGAAAAAGGCTAAGCA                  97308
```

```
; SEQ ID NO 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540

Alignment Scores:
Pred. No.:
Score:                 3.05e-49          Length:            99370
Percent Similarity:    560.00            Matches:           215
Best Local Similarity: 18.7%             Conservative:      1
Query Match:           18.6%             Mismatches:        5
DB:                    13.2%             Indels:            936
                       13.2%             Gaps:              2
                       3

US-09-855-828-1 (1-809) x US-09-949-016-17540 (1-99370)

Qy      589 ValPheGlyGluIleSerLeuLeuAlaAlaGlyLyGlyGlyAsnArgArgThrAlaAsnVal 608
                :::||||||||                   ||||||||||||||||||||
Db    93846 ATTTTTCTCTTACACGCCTTCTAGCAGCAGAGAGAAAACCGTCGAAACTGCCAATGTG 93905

Qy      609 ValAlaHisGlyPheAlaAsnLeuLeuThrLeuAspLysLysThrLeuGlnGluIleLeu 628
                ||||||||||||||||||||||||||||||||||||||
Db    93906 GTGGCCCACGGGTTTGCCAATCTTTTAACTCTAGACAACAAAAAGACCCTCCAAGAAATTCTA 93965

Qy      629 ValHisTyrProAspSerGluArgIleLeuMetLysLysLysAla------------ 642
                |||||||||||||||||||||||||||||||||||
Db    93966 GTGCATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAAGC-CAGGTACAACCTTTAAA 94024

Qy      642 ------------------------------------------------------------ 642
Db    94025 CACCATTAGAGATGGATGGGAGGTTGGTTTTTACTTTGTAAACTTCTGAGATAGGAGAACCGT 94084

Qy      642 ------------------------------------------------------------ 642
Db    94085 ATTATGATTGTGATAAAACTTGATCACAGTGAGATATGCTTAATGAACAACTATTAATGTA 94144

Qy      642 ------------------------------------------------------------ 642
Db    94145 GGTACCCATTGAAACTACACAGGTTAGGATAAATTGCAGTTTTTTTAGTAGATTTTGCCA 94204

Qy      643 -------------------------ArgValLeuLeuLys 647
                                         ||||||||||
Db    94205 GAAACTCTCACAGAGTTACCTAAAACAGCTTTTCTCTTTACCCACAGAGTGCTTTTAAAG 94264

Qy      648 GlnLysAlaLysThrLeuAlaThrProArgLysAspLeuAlaLeuLeuPhePro 667
                ||||||||||||||||||||||||||||||||||||||
Db    94265 CAGAGAGGCTAAGACCGGAGAAGCAAACCCCTCCAAGAAAAAGATCTTGCCCTCCTTCCCA 94324

Qy      668 ProLysGluGluThrProLysGlyPheLysThrLeuLeuGlyLyGlyThrGlyLysValaSer 687
                |||||||||||||||||||||||||||||||||||||||||||
Db    94325 CCGAAAAGAGAGAGGACACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGGAAAAGCAAGT 94384

Qy      688 LeuAlaArgLeuLeuLeuLysLeuArgGluGlnAlaAla---------------- 700
                ||||||||||||||||||||||||||||||||||||
Db    94385 CTTGCAAGACTACTCAAATTGAAGCGAGAGCAAGCAGC-TCAGGTAATAAAGGTGGGAGTGA 94443

Qy      700 ------------------------------------------------------------ 700
Db    94444 ATGGACGGCTGTCATGGAGAAGGCCCCAGAGACTAAGTATATACACAAAACGCCCACTCTA 94503

Qy      700 ------------------------------------------------------------ 700
Db    94504 ATTCCATTCAGACACTGGGATGATTTGGACTAATCTAATACTAATACTTCCTGCTTTAT 94563

Qy      700 ------------------------------------------------------------ 700
Db    94564 ATATAGCACATTATTATTTAAACTGCTGAATCCCACATATCATCACATTTAACCCTCAC 94623

Qy      700 ------------------------------------------------------------ 700
Db    94624 AGGATGTTTATAGATGGCTTTAATATGCATGTGTATTTATAAACAGAGTATACCCTCATTAT 94683
```

```
Db    94684 TCATAGATTATTTGCAGATTCTATATTGGTGAATCTACTTACTTATAATTTATTAGTAACT 94743
Qy      700 ------------------------------------------------------------ 700
Db    94744 TAAAATCAATACTCATGGTGCCTTTTGTGGTCATTTTGTGGACAACAGCACGTGCAGGGTGG 94803
Qy      700 ------------------------------------------------------------ 700
Db    94804 CAAAAAAATTTAAGTTGCTTGATGCATACACATTTTCAGCTCGAGTTTGAAAAAAGAGGCACTC 94863
Qy      700 ------------------------------------------------------------ 700
Db    94864 TCCTTTCTTGTTCAGCTCTGATACTATAAAACGAATGACCCTTGGCCGGGGGTGTGCGGTGGCT 94923
Qy      700 ------------------------------------------------------------ 700
Db    94924 CACACCTGTAATCCCAGCACTTTGGGAGGACCAAGGCGGGGGATCACGAGGGCGAGGAGAT 94983
Qy      700 ------------------------------------------------------------ 700
Db    94984 CGAGACCATTCTGACTAACACGGTGAAAACCCTGTCTCTACTGAAAACACAAAAAATTAGC 95043
Qy      700 ------------------------------------------------------------ 700
Db    95044 CGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTTGGGAGGCCGAAGGAATTG 95103
Qy      700 ------------------------------------------------------------ 700
Db    95104 CTTGAATCCGGGAGGAGGCAAAGGTTGTAGTGAGCCGAGATCACAACACTGCACTCCAGCCTG 95163
Qy      700 ------------------------------------------------------------ 700
Db    95164 GGGGACAGAGCAAATACTCTGTCTCAAAAAACAAAACAAAAACAACAAAAAA 95223
Qy      700 ------------------------------------------------------------ 700
Db    95224 AGAGTGACACTTTTAGGTGCCATGGCGTTTCCACATTTTTGTGCTTTGTGTGTGATT 95283
Qy      700 ------------------------------------------------------------ 700
Db    95284 TTGCTGCTTAAAAATAGCCCCCAAGCATAGTCGTTAGTGTTAGGTGAAACTTCATTCAGGC 95343
Qy      700 ------------------------------------------------------------ 700
Db    95344 CAAAATGCTGTGATGTGCCTTCCAGAGAAAATATGTGTTGTTAGGTAAACTTGTTACTGTGCTCCTTAAGTGC 95403
Qy      700 ------------------------------------------------------------ 700
Db    95404 ATTACAGTGCTGTTTGCATGAGTGTCAATATAATAATGAATCAAATTAATCCTCAAATTAATCAA 95463
Qy      700 ------------------------------------------------------------ 700
Db    95464 TTGATCAAATTAAATAGTGTATCTCTAAACACACAATGAAACAAAAGTTATACATT 95523
Qy      700 ------------------------------------------------------------ 700
Db    95524 GACCAAATTGACAAAAAATATTATGGCTTGAACCATAATATCTCATAGGAACCTAATGCTGT 95583
Qy      700 ------------------------------------------------------------ 700
Db    95584 ATTTCCTCCAAGAACAAATGGTTCAGTACTTGCTAACTTGCTGTTTGTGGAAAATTTATAG 95643
Qy      700 ------------------------------------------------------------ 700
Db    95644 AACAAAACTACATGAATAAAAATCAACTGTATATATACAGAACATACATATGGATATATAA 95703
Qy      700 ------------------------------------------------------------ 700
Db    95704 ATAAAATAACCCATTTTATCAACATTTTCACAAAATATTCAATTACTATAGATCACAAAATGT 95763
Qy      700 ------------------------------------------------------------ 700
```

```
Db  95764  TTAAAGCCCAAAAATAACTTTGTAAAATTTCATCCAAGCTTTTCATGTTATAGATGAAGAAA  95823
Qy    700  ------------------------------------------------------------    700
Db  95824  CTGAAAAACCAGATCAAGGGATTTGGATAAGATCACATAATTAGTTACAGAGCAGAAAGCTAT  95883
Qy    700  ------------------------------------------------------------    700
Db  95884  TACTCAGGTGTTCAGACTTACAGGCCTACACTAAGCTGCCTTTCAATTCCTAAAAATGTA  95943
Qy    700  ------------------------------------------------------------    700
Db  95944  AAGAAAACTCAAATGTTATTGTTTCTCTCTCTCTTTTTTTGGTTTCATATATTTC  96003
Qy    700  ------------------------------------------------------------    700
Db  96004  TTTGATTCTCATAATTAGCCTATGAGGGCAGATATTGAGAAAACAGACAGAGGGATTC  96063
Qy    700  ------------------------------------------------------------    700
Db  96064  AGGTTTTCTGAACCTAGTCATTATGTTATCTCTAAAACTGTAGAAATGGGTAGCTGTTGGA  96123
Qy    700  ------------------------------------------------------------    700
Db  96124  CCTTTCAGAAAATAAGTAAAGCACATATATTAATAAAGTCAGTCACATACAAAAGATGAAAAC  96183
Qy    700  ------------------------------------------------------------    700
Db  96184  TTGCATTTCCTTTTCCACACATACAACACTGTGTGGTGAAAGTTAGGGATCCAGTATAAAAC  96243
Qy    700  ------------------------------------------------------------    700
Db  96244  CAAATGCTTCATTTGCATCAGCCATAGAAATAATAATTTGCATAAAAAATGTATGGGAGTA  96303
Qy    700  ------------------------------------------------------------    700
Db  96304  AAGAAATATATAAGTAAAATGTGTTAAGAAATCTCAACTTTATCTGTGCACATTCATATGTC  96363
Qy    700  ------------------------------------------------------------    700
Db  96364  AGGCAAGCCTTTCTCAAATTGATCCCAAGCATTACCAGTAGTGTACCTTTTT  96423
Qy    700  ------------------------------------------------------------    700
Db  96424  GCTATGAGAAATTTCTATAGCTAGTGCTAAACACGATAGGTACAAACATGACAGGTCAAGCA  96483
Qy    700  ------------------------------------------------------------    700
Db  96484  CCTGTGGGACAAAATGGAAAAAGATCATACTAGGAAAGGGATAAGTTTCTCCCTGAGGTTCT  96543
Qy    700  ------------------------------------------------------------    700
Db  96544  CCCACAAGCTTAGGCAAGAGGAAAAACCCTACTTTTTACAGTATTTTTATATAGTAGTTGGT  96603
Qy    700  ------------------------------------------------------------    700
Db  96604  TAATATGTTTTATTAAAATAAATATTTATCTCTACAGAATAAGTAAATAT  96663
Qy    700  ------------------------------------------------------------    700
Db  96664  TTAAAAAGCAAAAACAGAGTCCTGACGCACTGAGTGTCTTAATATAATTCAGAGTATAAGCACC  96723
Qy    700  ------------------------------------------------------------    700
Db  96724  AATAGGAAGAGAATTCCTTGGCAGAGACAAAAAAAAATGCAATTCAGACTAACATCATGAGT  96783
Qy    700  ------------------------------------------------------------    700
Db  96784  CAAAGGCAACAAGTCCATTCTCTAGCACACCAGAAACTTCGTCAAATGATAGTACTCAGAAGC  96843
Qy    700  ------------------------------------------------------------    700
Db  96844  AAAGCAGAGACATGATTCCTCGATTCACTTAATTCAGAGACAGTCTGTCTCTTGGTGGTGAGATCTTA  96903
Qy    700  ------------------------------------------------------------    700
```

```
Qy    700  ------------------------------------------------------------    700
Db  96904  GCCATTGCATCGCTAATCAAAATCTAATCCAATGTTTTTAATTACGATTTCAACACCAGTT  96963
Qy    701  ----------------GlnLeuLysGlyGluAsnSerGluGlyGlyGlyLys  714
Db  96964  CTTTGTAATTGCTCCTTCCCAGAAGAAAATTCTGAAGGAGGAGGAGGAAAA  97023
Qy    715  GluAsnGluAspLysGlnLeuGlyGluAsnGluGlyGlyGly  734
Db  97024  GAAAATGAAGATAAACAAAAAGGAGAAAATGAAGGAGGAGGA  97083
Qy    735  LysGluAsnGluAspLysGlyAsnGluGlyGlyGly  754
Db  97084  AAAGAAAATGAAGATAAAGGAGAAAATGAAGGAGGAGGA  97143
Qy    755  GluCysThrAlaSerProIleAlaValGluGluGluProHisSerVal  774
Db  97144  GAATGTACAGCAAGTCCTATTGCAGTGGAGGAGGAACCCCACTCAGTTA  97203
Qy    775  LeuProArgGlyThrSerArgGlnSerLeuIleIleSerMetAlaProSerAlaGlyGly  794
Db  97204  TTACCCAGAGGGACTTCTCGTCAAATCACTCATTATCAGCATCGGC  97263
Qy    795  GlyGluGluValLeuThrIleGluValValLysGlyAlaLysGln  809
Db  97264  GGAGAAGAGGTTCTTACTATTGAAGTCAAAAGGAAAAGGCTAACCAA  97308
```

Alignment Scores:
Pred. No.:   1.8le-52
Score: 554.00
Percent Similarity: 99.1%
Best Local Similarity: 99.1%
Query Match: 13.1%
DB: 3

Length: 601
Matches: 108
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0

US-09-855-828-1 (1-809) x US-09-949-016-38931 (1-601)

```
Qy    701  GlnLeuLysGlyGluAsnSerGluGlyGlyGlyLysGluAsnGluAspLysGln  720
Db    464  CAGAGAGAAAGAAAATTCTGAAGGAGGAGGAGGAAAAGAAAATGAAGATAAACAA  405
Qy    721  LysGluAsnGluAspLysGlyAsnGluGlyGlyGlyLysGluAsnGluAspLys  740
Db    404  AAAGAAAATGAAGATAAAGGAAATGAAGGAGGAGGAAAAGAAAATGAAGATAAA  345
Qy    741  AspLysGlyAspArgGluProGluGlyLysProLeuAspArgProGluCysThrAlaSerPro  760
```

```
Db  344 GATAAAAGGAAGAGAGAGCCAGAAGAAGCCACTGGACAGACACTGRATGTRACAGGACGTCCT 285
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  761 IleAlaValGluGluGluProHisSerValArgArgThrValLeuProArgGlyThrSer 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  284 ATTGCAGTGGAGGAGAGAACCCCACTCAGTTRGAAGGACAGTTTTACCCGAGGGACTTCT 225

Qy  781 ArgGlnSerLeuIleIleSerMetAlaProSerAlaGluGluGlyGluGluValLeuThr 800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  224 CGTCAATCACTCATTATCAGCARTGGCATCCTTCTGAGGGCCGGAAGAGGTTCTTTACT 165

Qy  801 IleGluValLysGluLysAlaLysGln 809
            |||||||||||||||||||||||||||
Db  164 ATTGAGTCAAAGAAAAAGGCTAAGCAA 138
```

RESULT 15
US-09-949-016-205287/c

; Sequence 205287, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205287
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-205287

```
Alignment Scores:
Pred. No.:                           1.81e-52      Length:        601
Score:                  554.00                     Matches:       108
Percent Similarity:     99.1%                       Conservative:  0
Best Local Similarity:  99.1%                       Mismatches:    1
Query Match:            13.1%                        Indels:        0
DB:                     3                            Gaps:          0
```

US-09-855-828-1 (1-809) x US-09-949-016-205287 (1-601)

```
Qy  701 GlnLysLysGluAsnSerGluGlyGluGlyGluGlyLysGluAsnGluAspLysGln 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  464 CAGAAGAAAGAAAATTCTGAAGGAGAAGGAGAAGGAAAAGAAAAATGAAGATAAACAA 405

Qy  721 LysGluAsnGluAspLysGlnLysGlyGluGluAsnGluAspLys 740
            |||||||||||||||||||||||||||||||||||||||||||||
Db  404 AAAGAAAATGAAGATAAACAAAAAGGAGAAGAAAATGAAGATAAA 345

Qy  741 AspLysGlyArgGluProGluAspArgProGluCysThrAlaSerPro 760
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db  344 GATAAAGGAGAGCCAGAAGAGAGACCTGRATGTACAGCAAGTCCT 285

Qy  761 IleAlaValGluGluGluProHisSerValArgArgThrValLeuProArgGlyThrSer 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  284 ATTGCAGTGGAGGAGAGAACCCCACTCAGTTAGAAGGACAGTTTTACCCGAGGGACTTCT 225

Qy  781 ArgGlnSerLeuIleIleSerMetAlaProSerAlaGluGluGlyGluGluValLeuThr 800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  224 CGTCAATCACTCATTATCAGCATGGCATCCTTCTGAGGGCCGGAAGAGGTTCTTTACT 165

Qy  801 IleGluValLysGluLysAlaLysGln 809
            |||||||||||||||||||||||||||
Db  164 ATTGAGTCAAAGAAAAAGGCTAAGCAA 138
```

This Page Blank (uspto)

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2006 Bioacceleration Ltd.

GenCore version 5.1.8

Run on: May 18, 2006, 23:59:38 ; Search time 820 Seconds

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 atgttaaatcgctgacaaa.........aagaaaaggctaagcaataa 2430

Scoring table: IDENTITY NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
    1: /EMC_Celera_SIDS3/ptcdata/2/ina/1_COMB.seq:*
    2: /EMC_Celera_SIDS3/ptcdata/2/ina/5_COMB.seq:*
    3: /EMC_Celera_SIDS3/ptcdata/2/ina/6A_COMB.seq:*
    4: /EMC_Celera_SIDS3/ptcdata/2/ina/6B_COMB.seq:*
    5: /EMC_Celera_SIDS3/ptcdata/2/ina/7_COMB.seq:*
    6: /EMC_Celera_SIDS3/ptcdata/2/ina/H_COMB.seq:*
    7: /EMC_Celera_SIDS3/ptcdata/2/ina/PCTUS_COMB.seq:*
    8: /EMC_Celera_SIDS3/ptcdata/2/ina/PP_COMB.seq:*
    9: /EMC_Celera_SIDS3/ptcdata/2/ina/RE_COMB.seq:*
   10: /EMC_Celera_SIDS3/ptcdata/2/ina/backfiles1.seq:*

5544.871 Million cell updates/sec
(without alignments)

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2049.4	84.3	2135	3	US-09-949-016-1074	Sequence 1074, Ap
2	2035.4	83.8	2139	3	US-08-232-463-14	Sequence 14, Appl
3	330	13.6	99370	3	US-09-949-016-12816	Sequence 12816, A
4	330	13.6	99370	3	US-09-949-016-17540	Sequence 17540, A
5	329.6	13.6	601	3	US-09-949-016-38930	Sequence 38930, A
6	329.6	13.6	601	3	US-09-949-016-38931	Sequence 38931, A
7	329.6	13.6	601	3	US-09-949-016-205286	Sequence 205286, A
8	329.6	13.6	601	3	US-09-949-016-205287	Sequence 205287, A
9	202	8.3	601	3	US-09-949-016-205176	Sequence 205176, A
10	202	8.3	601	3	US-09-949-016-5678	Sequence 5678, Ap
11	181.2	7.5	2796	3	US-09-949-016-17420	Sequence 17420, A
12	169.8	7.0	84571	3	US-09-949-016-38897	Sequence 38897, A
13	151.4	6.2	601	3	US-09-949-016-205175	Sequence 205175, A
14	151.4	6.2	601	3	US-09-949-016-38915	Sequence 38915, A
15	147.6	6.1	601	3	US-09-949-016-205232	Sequence 205232, A
16	147.6	6.0	601	3	US-09-949-016-205228	Sequence 205228, A
17	144.6	6.0	601	3	US-09-949-016-205229	Sequence 205229, A
18	144.6	5.9	601	3	US-09-949-016-38929	Sequence 38929, A
19	143	5.9	601	3	US-09-949-016-205285	Sequence 205285, A
20	143	5.9	3470	3	US-09-949-016-4344	Sequence 4344, Ap
21	132.8	5.5	3470	3	US-09-949-016-16086	Sequence 16086, A
22	132.8	5.5	32666	3	US-09-949-016-38918	Sequence 38918, A
23	102.6	4.2	601	3		
24	102.6	4.2	601	3	US-09-949-016-205235	Sequence 205235,
25	93.8	3.9	7218	2	US-08-232-463-14	Sequence 14, Appl
26	91.4	3.8	601	3	US-09-949-016-38908	Sequence 38908, A
27	91.4	3.8	601	3	US-09-949-016-205201	Sequence 205201,
28	87	3.6	996	3	US-09-270-767-15059	Sequence 15059, A
29	85.6	3.5	2223	2	US-08-257-073-4	Sequence 4, Appli
30	79	3.3	1728	3	US-09-927-267-3	Sequence 3, Appli
31	79	3.3	2308	3	US-09-927-267-2	Sequence 2, Appli
32	79	3.3	2366	3	US-09-799-451-351	Sequence 351, App
33	78.8	3.3	929	3	US-09-671-317-14	Sequence 14, Appl
34	78	3.2	64309	3	US-09-949-016-14581	Sequence 14581, A
35	73.6	3.0	444	3	US-09-270-767-11944	Sequence 11944, A
36	73.6	3.0	7044	3	US-09-949-016-14113	Sequence 14113, A
37	72.8	3.0	1001	3	US-09-671-317-439	Sequence 439, App
38	72.8	3.0	4316	4	US-09-880-107-3713	Sequence 3713, Ap
39	72.6	3.0	1282	3	US-10-002-344A-89	Sequence 89, Appl
40	71	2.9	601	3	US-09-949-016-38919	Sequence 38919, A
41	71	2.9	601	3	US-09-949-016-205248	Sequence 205248,
42	70	2.9	88002	3	US-09-949-002-639	Sequence 639, App
43	70	2.9	88002	3	US-09-949-002-717	Sequence 717, App
44	68.2	2.8	3117	3	US-09-614-221A-275	Sequence 275, App
45	67.8	2.8	4167	3	US-09-973-278-700	Sequence 700, App

ALIGNMENTS

RESULT 1
US-09-949-016-1074
; Sequence 1074, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1074
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1074

Query Match   84.3%;   Score 2049.4;   DB 3;   Length 2135;
Best Local Similarity   99.2%;   Pred. No. 0;   Matches 2075;   Conservative   0;   Mismatches   1;   Indels   15;   Gaps   1;

Qy   340 CCACAAAAACAAACCGCCTGCAGCTCCTGTTGTTATAAAATGAGTATGCCGATGCCAGCTACAC 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCACAAAAACAAACCGCCTGCAGCTCCTGTTGTTATAAAATGAGTATGCCGATGCCAGCTAC 60

Qy   400 AACCTGGTGAAAAGAAATGCGTCAAAGAACAGCCCTCTACAAGAGAAAAGTTGGTAGAGGGA 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AACCTGGTGAAAAGAAATGCGTCAAAGAACAGCCCTCTACAAGAGAAAAGTTGGTAGAGGGA 120

Qy   460 GATCTTCTTCACCCGAAGCCAGCCCACAAAACTGCAAAAGCCAGGGCGTGTACCACCAGTA 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GATCTTCTTCACCCGAAGCCAGCCCACAAAACTGCAAAAGCCAGGGCGTGTACCACCAGTA 180

Qy   520 AAAGAAAAGCCGATGATAAGCCAACACAGAACAATTACTTACAGGCTGTTGTTGGTTCAAA 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAAGAAAAGCCGATGATAAGCCAACACAGAACAATTACTTACAGGCTGTTGTTGGTTCAAA 240

Qy   580 AAGATGCCCTTTAACAGAGTACTTAAAGCGAATTAAACTTCCAAACACAGCATAGAGTTCATAC 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db    241  AAGATGCCTTTAACAGAGACTACTTAAAGCGAATTAAACTTCCAAAACACGATAGATTCATAC  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241  AAGATGCCTTTAACAGAGACTACTTAAAGCGAATTAAACTTCCAAAACACGATAGATTCATAC  300

Db    301  ACAGATCGACTCTATCTCCCTGTGGCCTCTTGCTCACTCTTGCCTATAACTGGAACTGC  360
Qy    301  ACAGATCGACTCTATCTCCCTGTGGCCTCTTGCTCACTCTTGCCTATAACTGGAACTGC  360

Db    361  TGTTTTATACCACTGCGCGCCTCGTCTTCCCATATCAAACCGCAGACAACATACACTACTGG  420
Qy    361  TGTTTTATACCACTGCGCGCCTCGTCTTCCCATATCAAACCGCAGACAACATACACTACTGG  420

Db    421  CTTATTGCGGACATCATATGTGATATCATCTCACCTTTTATGATATGTCTATTTATCCAGCCC  480
Qy    421  CTTATTGCGGACATCATATGTGATATCATCTCACCTTTTATGATATGTCTATTTATCCAGCCC  480

Db    481  AGACTCCAGTTTGTTAAGAGGAGGAGACAATAATAGTGGATTCAAATGAGCTAAGGAAACAC  540
Qy    481  AGACTCCAGTTTGTTAAGAGGAGGAGACAATAATAGTGGATTCAAATGAGCTAAGGAAACAC  540

Db    541  TACAGGAGACTTCTACAAAATTTCAGTTGGATGTGCATCAATAATACCATTTGATATTTGC  600
Qy    541  TACAGGAGACTTCTACAAAATTTCAGTTGGATGTGCATCAATAATACCATTTGATATTTGC  600

Db    601  TACCTCTTCTTTCTTTGGGGTTTTAATCCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCA  660
Qy    601  TACCTCTTCTTTCTTTGGGGTTTTAATCCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCA  660

Db    661  TTTTTTGAATTTAAATCATCACCTAGAGTCTATAATGAACAAAGCATATATCTACAGAGTT  720
Qy    661  TTTTTTGAATTTAAATCATCACCTAGAGTCTATAATGAACAAAGCATATATCTACAGAGTT  720

Db    721  ATTCGAACAACTGGATACTTGCTGTGTTTATTCTGCACATTAATGCCCTGTGTTTATTACTGG  780
Qy    721  ATTCGAACAACTGGATACTTGCTGTGTTTATTCTGCACATTAATGCCCTGTGTTTATTACTGG  780

Db    781  GCTTCAAAACTATGAAGGAGAATTGGCACTACTACTAGATGGGTGTATCATGGAAGGAAACGAG  840
Qy    781  GCTTCAAAACTATGAAGGAGAATTGGCACTACTACTAGATGGGTGTATCATGGAAGGAAACGAG  840

Db    841  TATCTGAGATGTTATTATTGGGCAGTTCGAACTTTAATTACCATTGGTTGGCCTTCCAGRA  900
Qy    841  TATCTGAGATGTTATTATTGGGCAGTTCGAACTTTAATTACCATTGGTTGGCCTTCCAGRA  900

Db    901  CCACAAAACTTTATTTGAAATTGTTTTTCAACTCTTGAATTTTTTCTGGAGTTTTTTGTG  960
Qy    901  CCACAAAACTTTATTTGAAATTGTTTTTCAACTCTTGAATTTTTTCTGGAGTTTTTTGTG  960

Db    961  TTCTCCAGTTTAATTGGTCAGATGAGATGTGATTGGAGCGAGCAATCAGAAC  1020
Qy    961  TTCTCCAGTTTAATTGGTCAGATGAGATGTGATTGGAGCGAGCAATCAGAAC  1020

Db   1021  TACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGTAACAAATTACTCCATTCCTAAA  1080
Qy   1021  TACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGTAACAAATTACTCCATTCCTAAA  1080

Db   1081  CTTGTGCAAAAGCGAGTTCGGACTTGGTTGTATGATATACATGGGAACTTCTCAAAGAAATGCTA  1140
Qy   1081  CTTGTGCAAAAGCGAGTTCGGACTTGGTTGTATGATATACATGGGAACTTCTCAAAGAAATGCTA  1140

Db   1141  GATGAGTCTGATTTGCTTAAGACCCTACCAACTACGGTTCAAGGGTTGTGATACACAGATGATT  1200
Qy   1141  GATGAGTCTGATTTGCTTAAGACCCTACCAACTACGGTTCAAGGGTTGTGATACACAGATGATT  1200

Db   1201  GTGAACTTCAGCATCATCAGCAAAGTCGGACTTGTTCAAGGGTTGATACACAGATGATT  1260
Qy   1201  GTGAACTTCAGCATCATCAGCAAAGTCGGACTTGTTCAAGGGTTGATACACAGATGATT  1260

Db   1261  TATGACATGTTGCTAAGATTGAAAATCCGTTCCCTCTATTTGCCTCGGTGACTTTGTCTGCAAA  1320
Qy   1261  TATGACATGTTGCTAAGATTGAAAATCCGTTCCCTCTATTTGCCTCGGTGACTTTGTCTGCAAA  1320

Db   1321  AAGGGAGAAATTGGCAAGGAAATGTATATCATCAAGCATGGAGGAGAGTCCAAGTTCTTGGA  1380
Qy   1321  AAGGGAGAAATTGGCAAGGAAATGTATATCATCAAGCATGGAGGAGAGTCCAAGTTCTTGGA  1380

Db   1381  GGCCCTGATGGTACTAAAGTTCTTGGTTTACTTCTGGAAAAGCTGGGTGGTTTGGAGAAATC  1427
Qy   1381  GGCCCTGATGGTACTAAAGTTCTTGGTTTACTTCTGGAAAAGCTGGGTCGGTGTTTGGAGAAATC  1380

Db   1428  --CCTTCTAGCACGCAGGAGGAGGAGGAGAAACCGTCGAAACTGCCAAATGTGGGTGGCCCACGGGTTT  1485
Qy   1428  AGCCTTCTAGCACGCAGGAGGAGGAGGAAACCGTCGAAACTGCCAAATGTGGGTGGCCCACGGGTTT  1839

Db   1486  GCCAAATCTTTTAACTCTAGACAAAAGAAGGACCCCTCCAAGAAAATTCTAGTCATTTATCCAGAT  1545
Qy   1486  GCCAAATCTTTTAACTCTAGACAAAAGAAGGACCCCTCCAAGAAAATTCTAGTCATTTATCCAGAT  1545

Db   1546  TCTGAAAAGGATCCTCATGAAGAAAAGCCAGAGTGCTTTTAAAGCAGAAGGAGGGACCCGCA  1605
Qy   1546  TCTGAAAAGGATCCTCATGAAGAAAAGCCAGAGTGCTTTTAAAGCAGAAGGAGGGACCCGCA  1605

Db   1606  GAAGCAACCCCTCCAAGAAAAGAATCTTGCCCTCCTCCTCCCACCGAAAAGAAAGAGAGACACCC  1665
Qy   1606  GAAGCAACCCCTCCAAGAAAAGAATCTTGCCCTCCTCCTCCCACCGAAAAGAAAGAGAGACACCC  1665

Db   1666  AAACTGTTTAAAAACTCTCCTAGGAGGCACAGGAAAGCAAGTCTTGCAAGACTACTCAAA  1725
Qy   1666  AAACTGTTTAAAAACTCTCCTAGGAGGCACAGGAAAGCAAGTCTTGCAAGACTACTCAAA  1725

Db   1726  TTGAAGCCAGAGCCAAGCAGCTCAGAAGAAGCAGCTCAGAAAAATTCTGAAGGAGGGAAGGAGGA  1785
Qy   1726  TTGAAGCCAGAGCCAAGCAGCTCAGAAGAAGCAGCTCAGAAAAATTCTGAAGGAGGGAAGGAGGA  1785

Db   1786  AAAGAAAAATGAAGATAAAACAAAAAAGAAAAATGAAGATAAAAGAAGAAAATGAAGAATAA  1845
Qy   1786  AAAGAAAAATGAAGATAAAACAAAAAAGAAAAATGAAGATAAAAGAAGAAAATGAAGAATAA  1845

Db   1846  GGAAAAGAAAAATGAAGATAAAAGAAGAGAGCCCAGAAGACCCACTGGGACACAGA  1905
Qy   1846  GGAAAAGAAAAATGAAGATAAAAGAAGAGAGCCCAGAAGACCCACTGGGACACAGA  1905

Db   1906  CCTGAAATGTACACGCAAGTCCTATTGCACGTGGGAGGAGAGAGAACCCCACTCAGTTAGAAGGACA  1965
Qy   1906  CCTGAAATGTACACGCAAGTCCTATTGCACGTGGGAGGAGAGAGAACCCCACTCAGTTAGAAGGACA  1965

Db   1966  GTTTTACCCGAGGGGACTTCTCGGTCAATCACTCATTATCAGAGCAAGTGGCTCCTTGCTGAG  2025
Qy   1966  GTTTTACCCGAGGGGACTTCTCGGTCAATCACTCATTATCAGAGCAAGTGGCTCCTTGCTGAG  2379

Db   2026  GGGGGAGAAGAGAGGTTCTTACTATTGAAGTCAAAAGAAAAAGGCTAAGCAATAA  2076
Qy   2380  GGGGGAGAAGAGAGGTTCTTACTATTGAAGTCAAAAGAAAAAGGCTAAGCAATAA  2430
```

```
; ORGANISM: Human
US-09-949-016-5798

Query Match      83.8%;  Score 2035.4;  DB 3;  Length 2139;
Best Local Similarity  99.0%;  Pred. No. 0;  Mismatches 1;  DB 3;  Indels 19;  Gaps 2;
Matches 2075;  Conservative  0;  Mismatches  1;  Indels  19;  Gaps  2;

Qy    340  CCACAAAACAAAACCGCCTGCAGCTCCTGTTATAAAATGAGTAATGCCGATGCCCAGCTACAC   399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CCACAAAACAAAACCGCCTGCAGCTCCTGTTATAAAATGAGTAATGCCGATGCCCAGCTACAC    60

Qy    400  AACCTGGTGAAAAGAATGCGTCAAAAGAACAGCCCTCTACAAGAGAAAGAAAGTTGGGTGAGGGA   459
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AACCTGGTGAAAAGAATGCGTCAAAAGAACAGCCCTCTACAAGAGAAAGAAAGTTGGGTGAGGGA   120

Qy    460  GATCTCTTCCTCACCCCAACACTGCAAAAGCCCCACCGGGTGCTACCACAGTA   519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GATCTCTTCCTCACCCCAACACTGCAAAAGCCCCACCGGGTGCTACCACAGTA   180

Qy    520  AAAGAAAAGCGATTGATAAGCCAACAGAACATTACTACAGAGTCAAA   579
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    181  AAAGAAAAGCGATTGATAAGCCAACAGAACATTACTACAGAGTCAAA   240

Qy    580  AAGATGCCTTTAAACAGATACTTAAACGAATTAAACTTCCAAACAGAATAGAGTTCATTAC   639
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AAGATGCCTTTAAACAGATACTTAAACGAATTAAACTTCCAAACAGAATAGAGTTCATTAC   300

Qy    640  ACAGATCGACTCTATCCTCCTGTGGCCTCTTGCTTGTCTGCCTATAACTGGACTGC   699
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  ACAGATCGACTCTATCCTCCTGTGGCCTCTTGCTTGTCTGCCTATAACTGGACTGC   360

Qy    700  TGGTTTATACCACTGGGCCTCGTCTTCCCATATCAAACCGCAGACAACATACACTACTGG   759
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TGGTTTATACCACTGGGCCTCGTCTTCCCATATCAAACCGCAGACAACATACACTACTGG   420

Qy    820  AGACTCCAGTTTGTAGGAGGAGCATAATAGTGGATTCAAATAGTGAGCTAAGGAGAAACAC   879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AGACTCCAGTTTGTAGGAGGAGCATAATAGTGGATTCAAATAGTGAGCTAAGGAGAAACAC   540

Qy    880  TACAGGACTTCTACAAAATTTCAGTTGGGATGGTCGCATCAATAATACCATTGAATAATTGC   939
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TACAGACTTCTCCAAAATTTCAGTTGGGATGTTCGCATCAATAATACCATTGAATAATTGC   600

Qy    940  TACCTCTTCTTTGGGTTTAATCCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCA   999
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TACCTCTTCTTTGGGTTTAATCCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCA   660

Qy   1000  TTTTTTTGAATTTAATCATCACCTACCTGAGTCTTATATATGGACAAAGCCCATATATCTACACAGTT  1059
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TTTTTTTGAATTTAATCATCACCTACCTGAGTCTTATATATGGACAAAGCCCATATATCTACACAGTT   720

Qy   1060  ATTCGAACAACTGGATACTTGCCTGTCTGTTTATTCTGCACATTAATCATTTATTACTGG  1119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATTCGAACAACTGGATACTTGCCTGTCTGTTTATTCTGCACATTAATCATTTATTACTGG  780

Qy   1120  GCTTCAAACTATGAAGGAAATTGGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAG  1179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GCTTCAAACTATGAAGGAAATTGGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAG  840

Qy   1180  TATCTGAGATGTTATTTATTTGGGCAGTTGGCCTTCCCTTTAATTAACATTGGTGTGGCCTTGCCTTCCAGAA  1239
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TATCTGAGATGTTATTTATTTGGGCAGTTGGCCTTCCCTTTAATTAACATTGGTGTGGCCTTGCCTTCCAGAA  900

Qy   1240  CCACAAAACTTTATTTGAAAATTGTTTTTTTCAACCTTGAAATTTTTTTTCTGGAGTTTTTGTG  1299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CCACAAAACTTTATTTGAAAATTGTTTTTTTCAACCTTGAAATTTTTTTTCTGGAGTTTTTGTG  960

Qy   1300  TTCTCCAGTTTAATTGGTCAGATGAGAGAGTGTTGATTGGGACGAGCTACAGCCAATCAGAAC  1359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTCTCCAGTTTAATTGGTCAGATGAGAGAGTGATTGAGTGAGCAGCTACAGCCAATCAGAAC  1020
```

```
Db    961  TTCTCCAGTTTAATTGGTCAGATGAGAGAGTGATTGAGTGAGCAGCTACAGCCAATCAGAAC  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360  TACTTCCCGGCGCCTGCATGGATGACCACCATTGCCTACCATGAAGCAATTACTTCCAATTTCCTAAA  1419

Db   1021  TACTTCCCGGCGCCTGCATGGATGACCACCATTGCCTACCATGAAGCAATTACTTCCAATTTCCTAAA  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420  CTTGTGCAAAAAGGCAGAGTTCGGACTTGGTATGATATACATGCAGACTCTCAAAAGAATTGCTA  1479

Db   1081  CTTGTGCAAAAAGGCAGAGTTCGGACTTGGTATGATATACATGCAGACTCTCAAAAGAATTGCTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480  GATGAGTGTCTGATTTGCTTTAAGACCCTACCAACTACGGTCCAGTTGAGCCCTTCGCCATTTGAT  1539

Db   1141  GATGAGTGTCTGATTTGCTTTAAGACCCTACCAACTACGGTCCAGTTGAGCCCTTCGCCATTTGAT  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540  GATTTATGACATGTTGCTTAAGATTGAAATCCGTTCTCTATTTGTCTTGTGTTGTGTCTG  1595
```

RESULT 3
US-09-016-12816
; Sequence 12816, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 12816
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12816

Query Match   13.6%; Score 330; DB 3; Length 99370;
Best Local Similarity 100.0%; Pred. No. 2.4e-70;
Matches 330; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2101 CAGAGAAAGAAAGAAATTCTGAAGGAGGAGGAGGAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAAACA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96982 CAGAGAAAGAAAGAAATTCTGAAGGAGGAGGAGGAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAAACA 97041

Qy   2161 AAAGAAAATGAAGAGATAAAACAAAAGAAAAAGAAAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAA 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97042 AAAGAAAATGAAGAGATAAAACAAAAGAAAAAGAAAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAA 97101

Qy   2221 GATAAAAGGAAGAGAGCCAGAGGACAGAGAGCCACTGGACAGAGACCTGAATGTACAGCAAGTCCT 2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97102 GATAAAAGGAAGAGAGCCAGAGGACAGAGAGCCACTGGACAGAGACCTGAATGTACAGCAAGTCCT 97161

Qy   2281 ATTGCAGTGGAGGAAGAAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCT 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97162 ATTGCAGTGGAGGAAGAAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCT 97221

Qy   2341 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTGCTGAGGGCGGAGAAGAGGACTTACT 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97222 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTGCTGAGGGCGGAGAAGAGGACTTACT 97281

Qy   2401 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 2430
           |||||||||||||||||||||||||||||||
Db   97282 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 97311

RESULT 4
US-09-016-17540
; Sequence 17540, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540

Query Match   13.6%; Score 330; DB 3; Length 99370;
Best Local Similarity 100.0%; Pred. No. 2.4e-70;
Matches 330; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2101 CAGAGAAAGAAAGAAATTCTGAAGGAGGAGGAGGAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAAACA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96982 CAGAGAAAGAAAGAAATTCTGAAGGAGGAGGAGGAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAAACA 97041

Qy   2161 AAAGAAAATGAAGAGATAAAACAAAAGAAAAAGAAAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAA 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97042 AAAGAAAATGAAGAGATAAAACAAAAGAAAAAGAAAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAA 97101

Qy   2221 GATAAAAGGAAGAGAGCCAGAGGACAGAGAGCCACTGGACAGAGACCTGAATGTACAGCAAGTCCT 2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97102 GATAAAAGGAAGAGAGCCAGAGGACAGAGAGCCACTGGACAGAGACCTGAATGTACAGCAAGTCCT 97161

Qy   2281 ATTGCAGTGGAGGAAGAAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCT 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97162 ATTGCAGTGGAGGAAGAAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCT 97221

Qy   2341 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTGCTGAGGGCGGAGAAGAGGACTTACT 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97222 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTGCTGAGGGCGGAGAAGAGGACTTACT 97281

Qy   2401 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 2430
           |||||||||||||||||||||||||||||||
Db   97282 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 97311

RESULT 5
US-09-016-38930/c
; Sequence 38930, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38930
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38930

Query Match   13.6%; Score 329.6; DB 3; Length 601;
Best Local Similarity 99.7%; Pred. No. 3.5e-71;
Matches 329; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   2101 CAGAGAAAGAAAGAAATTCTGAAGGAGGAGGAGGAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAAACA 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   414 CAGAGAAAGAAAGAAATTCTGAAGGAGGAGGAGGAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAAGAGATAAAACA 355

Qy   2161 AAAGAAAATGAAGAGATAAAACAAAAGAAAAAGAAAGGAGGAGGAAGAAGAAAAGAAAGAAAATGAARGATAAA 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db   354 AAAGAAAATGAAGAGATAAAACAAAAGAAAAAGAAAGGAGGAGGAAGAAGAAAAGAAAGAAAATGARGATAAA 295

Left column

```
Qy   2221 GATAAAGGAAGAGAGAGCCAGAAGAGAAGAAGCCACTGGACAGCTGAAATGTACAGCAAGTCCT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 GATAAAGGAAGAGAGAGCCAGAAGAGAAGAAGCCACTGGACAGCTGAAATGTACAGCAAGTCCT  235

Qy   2281 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGAAGGACAGTTTTACCCAGAGGGGACTTCT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGAAGGACAGTTTTACCCAGAGGGGACTTCT  175

Qy   2341 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTTCTGCTGAGGGGCGGAGAAGAGGTTCTTACT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    174 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTTCTGCTGAGGGGCGGAGAAGAGGTTCTTACT  115

Qy   2401 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 2430
          |||||||||||||||||||||||||||||||
Db    114 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA   85
```

RESULT 6
US-09-949-016-38931/c
Sequence 38931, Application US/0994901c
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38931
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38931

Query Match   13.6%;
Best Local Similarity   99.7%;
Matches 329; Conservative 1; Mismatches 0;

Score 329.6; DB 3; Length 601;
Pred. No. 3.5e-71; Indels 0; Gaps 0;

```
Qy   2101 CAGAAGAAAGAAAAATTCTGAAGGAGGAAGAGAAGAGGAGAAAGAAGATAAACAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 CAGAAGAAAGAAAAATTCTGAAGGAGGAAGAGAAGAGGAGAAAGAAGATAAACAA  405

Qy   2161 AAAGAAAAATGAAGATAAACAAAAAAGAAAGAAAAATGAAGATAAA 2220
          |||||||||||||||||||||||||||||||||||||||||||||
Db    404 AAAGAAAAATGAAGATAAACAAAAAAGAAAGAAAAATGAAGATAAA  345

Qy   2221 GATAAAGGAAGAGAGAGCCAGAAGAGAAGAAGCCACTGGACAGCTGAAATGTACAGCAAGTCCT 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 GATAAAGGAAGAGAGAGCCAGAAGAGAAGAAGCCACTGGACAGCTGAAATGTACAGCAAGTCCT  285

Qy   2281 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGAAGGACAGTTTTACCCAGAGGGGACTTCT 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGAAGGACAGTTTTACCCAGAGGGGACTTCT  225

Qy   2341 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTTCTGCTGAGGGGCGGAGAAGAGGTTCTTACT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    224 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTTCTGCTGAGGGGCGGAGAAGAGGTTCTTACT  165

Qy   2401 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 2430
          |||||||||||||||||||||||||||||||
Db    164 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA  135
```

RESULT 7

Right column

US-09-949-016-205286/c
Sequence 205286, Application US/0994901c
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205286
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205286

Query Match   13.6%;
Best Local Similarity   99.7%;
Matches 329; Conservative 1; Mismatches 0;

Score 329.6; DB 3; Length 601;
Pred. No. 3.5e-71; Indels 0; Gaps 0;

```
Qy   2101 CAGAAGAAAGAAAAATTCTGAAGGAGGAAGAGAAGAGGAGAAAGAAGATAAACAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 CAGAAGAAAGAAAAATTCTGAAGGAGGAAGAGAAGAGGAGAAAGAAGATAAACAA  355

Qy   2161 AAAGAAAAATGAAGATAAACAAAAAAGAAAGAAAAATGAAGATAAA 2220
          ||||||||||||||||||||||||||||||||||||| |||||||
Db    354 AAAGAAAAATGAAGATAAACAAAAAAGAAAGAAAAATGAAGARGATAAA  295

Qy   2221 GATAAAGGAAGAGAGAGCCAGAAGAGAAGAAGCCACTGGACAGCTGAAATGTACAGCAAGTCCT 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 GATAAAGGAAGAGAGAGCCAGAAGAGAAGAAGCCACTGGACAGCTGAAATGTACAGCAAGTCCT  235

Qy   2281 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGAAGGACAGTTTTACCCAGAGGGGACTTCT 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGAAGGACAGTTTTACCCAGAGGGGACTTCT  175

Qy   2341 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTTCTGCTGAGGGGCGGAGAAGAGGTTCTTACT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    174 CGTCAATCACTCATTATCAGCATGGCTCCTTCCTTCTGCTGAGGGGCGGAGAAGAGGTTCTTACT  115

Qy   2401 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA 2430
          |||||||||||||||||||||||||||||||
Db    114 ATTGAAGTCAAAGAAAAAGGCTAAGCAATAA   85
```

RESULT 8
US-09-949-016-205287/c
Sequence 205287, Application US/0994901c
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205287

```
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-205287

Qy      Query Match          13.6%;
        Best Local Similarity     99.7%;
        Matches  329; Conservative    1; Pred. No. 3.5e-71;

Qy   2101 CAGAAGAAGAAAGAAAATTCTGAAGGAGGAGGAGGAAGAAGAAGAAGAAGAAGAATGAAGAATAAACA 2160
          |||||||||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 CAGAAGAAAGAAAATTCTGAAGGAGGAGGAGGAAGAAGAAGAAGAAGAAGAATGAAGAATAAACA 405

Qy   2161 AAAGAAAATGAAGAATAAACAAAAAGAAAAGAAAATGAAGAAGAAGAAGAAAATGAAGAATAAA 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 AAAGAAAATGAAGAATAAACAAAAAGAAAAGAAAATGAAGAAGAAGAAGAAAATGAAGAATAAA 345

Qy   2221 GATAAAAGGAAGAGAGCCAGAAGAAGAACCACTCGAATCGTACAGCAAGTCCT 2280
          |||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    344 GATAAAAGGAAGAGAGCCAGAAGAAGAACCACTCGRATGTACAGCAAGTCCT 285

Qy   2281 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACACAGTTTTACCCAGAGGGGACTTCT 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACACAGTTTTACCCAGAGGGGACTTCT 225

Qy   2341 CGTCAATCACTCATTATCAGCAATGGCTCCCTTCGTGAGGGGCCGGAGGAAGGAGAGGTTCTTACT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    224 CGTCAATCACTCATTATCAGCAATGGCTCCCTTCTTCTGCGTGAGGGGCGGAGAAGGAGAGGTTCTTACT 165

Qy   2401 ATTGAAGTCAAAAGAAAAGGCTAAGCAATAA 2430
          |||||||||||||||||||||||||||||||
Db    164 ATTGAAGTCAAAAGAAAAGGCTAAGCAATAA 135

RESULT 9
US-09-949-016-38898/c
;   Sequence 38898, Application US/09949016
;   Patent No. 6812339
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE:  2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE:  2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE:  2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE:  2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 38898
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-38898

Qy      Query Match           8.3%;       Score 202;  DB 3;  Length 601;
        Best Local Similarity   100.0%;   Pred. No. 8.6e-40;
        Matches  202; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy    641 CAGATCGACTCTATCTCCTGTGGGCCTCTTGCTTGTCACTCTTGCCTATAACTGGAACTGCT 700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 CAGATCGACTCTATCTCCTGTGGGCCTCTTGCTTGTCACTCTTGCCTATAACTGGAACTGCT 143

Qy    701 GGTTTATACCACTCGCGCCCTCGCTCTTCCCATATCAAACCGGAGACAACATACACTACTGGC 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GGTTTATACCACTCGCGCCCTCGCTCTTCCCATATCAAACCGGAGACAACATACACTACTGGC 83

Qy    761 TTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCCA 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 TTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCCA 23
```

```
Db     82 TTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCCA 23
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    821 GACTCCAGTTTGTAAGAGGAGG 842

Db     22 GACTCCAGTTTGTAAGAGGAGG 1

RESULT 10
US-09-949-016-205176/c
;   Sequence 205176, Application US/09949016
;   Patent No. 6812339
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE:  2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE:  2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE:  2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE:  2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 205176
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-205176

Qy      Query Match           8.3%;       Score 202;  DB 3;  Length 601;
        Best Local Similarity   100.0%;   Pred. No. 8.6e-40;
        Matches  202; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy    641 CAGATCGACTCTATCTCCTGTGGGCCTCTTGCTTGTCACTCTTGCCTATAACTGGAACTGCT 700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 CAGATCGACTCTATCTCCTGTGGGCCTCTTGCTTGTCACTCTTGCCTATAACTGGAACTGCT 143

Qy    701 GGTTTATACCACTCGCGCCCTCGCTCTTCCCATATCAAACCGGAGACAACATACACTACTGGC 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GGTTTATACCACTCGCGCCCTCGCTCTTCCCATATCAAACCGGAGACAACATACACTACTGGC 83

Qy    761 TTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCCA 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 TTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCCA 23

Qy    821 GACTCCAGTTTGTAAGAGGAGG 842
          |||||||||||||||||||||
Db     22 GACTCCAGTTTGTAAGAGGAGG 1

RESULT 11
US-09-949-016-5678
;   Sequence 5678, Application US/09949016
;   Patent No. 6812339
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE:  2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE:  2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE:  2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE:  2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 5678
```

```
;  LENGTH: 2796
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-5678

Query Match    49.8%;  Score 181.2;  DB 3;  Length 2796;
Best Local Similarity   49.8%;
Matches  620;  Conservative  0;  Mismatches  588;  Indels  36;  Gaps  5;

Qy      740 CAGACACATACACTACCTGGCTTTATTGGGGACATCATCATATGTGATATCATCTACCTTTATG 799
            ||| ||   ||| ||| | |||||| |  ||| |   ||  | || ||  |  ||   |||||
Db      897 CTGATTACCTAGAAATAATTGGCTCATTTTTGGATGTATCAGACACATAGTCTATTTAATCG 956

Qy      800 ATATGCTATTTATCCAGCCCAGACTCCAGTTTGTTAAGAGGAGGACATAATAGTGGATT 859
            | | |||  ||||| ||  |  || ||||| ||| | ||| || || || |  ||||||
Db      957 ATATG---TTTGTACGAACAAGGACAGGTTACCTAGAACAAGGACTGCTGGTAAAGGAAG 1013

Qy      860 CAAATGAGCTAAGGAAAACACTACAGGACTTCTACAAAATTTCAGTTGGATGTGCCATCA 919
            |||||||  ||||||| || ||||| ||||||| ||  |||||||||||||| || |||
Db     1014 AACTTAAAACTCATAAAATATAAAATCCAAACTTGCAATTAAACTTGAITGTTCTGTCAC 1073

Qy      920 TAATACCATTTGATATTTGTTACCTCTTCTTTGGGTTTA---ATCCAAATGTTTAGAGCAA 976
            | |||| ||| || | || |  || | ||| |||||||    ||||||  |  |||||||
Db     1074 TGATACCAACTGATTTGCTGTATTTTAAGTTAGGGTGGAACTATCCAGAAATTAGATTA 1133

Qy      977 ATAGGAGTGTTAAAGTACACTTCATTTTTTGAATTAATCATCACTGAGTCTATAATGG 1036
            || ||| || | | |||| ||||| | ||||  ||| |  |||| || | || ||||
Db     1134 ACAGGTTGTTACGGTTCTCTCGTATGTTTGAGTTCTTCACAGAAACAAGGACAA 1193

Qy     1037 ACAAAGCATATATCTACACAGAGTTATTCGAACAACTGGGATACTTGCTGTTTATTCTGCACA 1096
            ||| | || || ||  | ||| | |  |||||||| | ||||| |||| ||| || ||||||
Db     1194 ACTATCCAAACATCTTCAGGAATTCCAACCTTGTTATGTTTTATGTCGATTCATCATTAATCG 1253

Qy     1097 TTAATGCCTGTGTTTATTATTACTGGGCTTCAAACTATATGAAGGAATTGGGCACTACTAGATGGG 1156
            ||  || || | ||| |||||| | ||| | | |  |  ||| | |||| | || |||||||
Db     1254 GGAATGCATGTGTGTTCTACTCTATTTCTAAAGCTATTGGATTTTGAAATGAACATATGGG 1313

Qy     1157 TGTA-----------TGATGGGGAAGGAAAACGAGTTATCTGAGATGTT 1192
            ||                ||||  ||| ||  || |  |  || ||| |
Db     1314 TCTACCCTGATATTAATGATCCTGAATTTGCCGTTTCGGCTTAGAAAATACGTATACAGCC 1373

Qy     1193 ATTATTGGGCAGTTCGAACTTTAATTACCATTGGTGTGGCCTTCCAGGAACCACAAAACTTTAT 1252
            |||||||  ||| | || ||||| || ||| ||||||||  ||| | ||| |  ||||||
Db     1374 TTTACTCGGTCTACACTGACTTTGACTACCATTGGTGAAACACCCCCTCCCGTGAGGGATT 1433

Qy     1253 TTGAAAATTGTTTTTCAACTCTTGAAATTTTTTTTGTTGGTTCTCCAGTTTTAA 1312
            || | || ||||  |  ||| |||| | ||||| || |||| | |||||||||
Db     1374 TTTACTCGGTCTACACTGACTTTGACTACCATTGGTGAAACACCCCCTCCCGTGAGGGATT 1433

Qy     1313 TTGGTCAGATGAGAGAATGTGATTGGAGCAGCCAAATCAGAGAACTACTTCCGCGCCT 1372
            | || || | | | ||| | || ||| |   ||  |||  ||  ||| ||  | |||
Db     1434 CTGAGTAGTGTCTTTGTGGGTGGTTCATTTCCTAATTGGACGTGTTTTAATTTTTGCTACCATCG 1493

Qy     1373 GCATGGATGACACCATTGCCTACACTGAACATGCAGCAAGCAGAATTCAAGCTAGAAAGC 1432
            ||| || |  ||| || | ||| || ||  |||| | |  ||| |  ||   |||||
Db     1494 TTGGTACACATGACGTTCTATGATTCCAACACATGCAGCAGAATTACTTCAAGCAA 1553

Qy     1433 GAGTTCGGACTTGGTATGAATATACATGGGACACTCTCAAAGAGAATGCTAGATGTGTCGATT 1492
            ||||  || | |  | ||| | |  ||| |||| | | ||| | |  | | |||| | |||
Db     1554 GAATTGATGCTATCAAGCAATAATATATGCATTTTTCGAAAATGTAAGCAAAGATAGGAAAAAGA 1613

Qy     1493 TGCTTAAGACCCCTACCAACTACGGGTCCACAGTTAGCCTCGCCATTGATGATGAACTTCAGCA 1552
            || |  || ||| | ||| ||||| ||||  |||  |||| | | || | || |||| |||
Db     1614 GGGTTATTAAATGGTTTGACTACCTGCCACAACAAAAACAGTTGTAGATGAGAAAGAAG 1673

Qy     1553 TCATCAGCAAAGTCGACTTGTTCAAGGGGTTGTGATACACAGATCAATTTATGACAGTGTGC 1612
            ||| |   | || ||| || ||     ||| || | |  |||||| | |||| | ||||
Db     1674 TCTTAAAGTATCCTGATAAACTAGAAGAGCAGAAAATTGCCATCAAACGTTCAACTGTTGCA 1733

Qy     1613 TAAGATTGAAAATCCGTTCTCTATTTGCCTGGGTCTGCAAAAAAAGGGGAGAAAATTG 1672
            |   || |||| ||| |  | ||| | || | |||| ||   || |||||  ||||||
Db     1734 CATTAAAAAAGGTACGACCATTTTTGCCTGATTGTGAAGCTCGGTCTTGGTGAGTTGGGTCT 1793

Qy     1673 GCAGGGAAATGTATATCATCAAAGCCATGGAGAAGTCCAAGTTCTTGGAGGCCCCTGATTG 1732
            ||| ||| |   | ||| || | |  |||  |||| | ||| ||||  |||| | |||| |
Db     1854 GACGAGAGATGTACATTATCAGCCATGAGTAGCAAGTGCTAGTCC 1913

Qy     1733 CTAAAGTTCTGGT-----TACTCTGAAAGCTGGGTCGGGTGTTTTGGGAGAAATC 1786
            |  ||||| | |     ||  |||||| | |||||  || ||   |  ||||  |
Db     1914 CTCAGTTGTTGGTATTGACGGAATGGCCAGCTACTTCGGGTGAGACATCGGAAATCGGAGACC 1973

Qy     1787 TAGCAGCAGGAGGAGGAGAAACCGTCGAACTCCAAGTGTGGGTGCCCACGGGTTTGCCAATC 1846
            |  ||| | || || | |  || || || ||||   ||| | | ||  | |||  || | |
Db     1974 AAGGGAGCGAAAGCTGGCAATCGACGGATGGCATCAGATATTTAAAGTATTGGGTTACTCAGACC 2033

Qy     1847 TTTTAACTCTTAGACAAAAAGACCCTCCAGAAATTCATAGTGCATTATCCAGATTCTGAAA 1906
            |||| || ||| | |||| | ||   | |||   | |||| || |||| |||| | |||
Db     2034 TGTTCTGTCTCTCAAAAGATGACCTCATGGAAGCTCTAACTGACTGAGTGCCAAAA 2093

Qy     1907 GGATCCTCATGAAGAGAAAAGCCAGAGTGCTTTTAAGGAGGGGCT 1950
            ||| | |   | ||||||||  |||| | | ||||| ||||| |
Db     2094 CTATGCTGGAAGAGAGAAAGGGGAAGCAGATTTTAATGAAAAGATGGT 2137
```

```
RESULT 12
US-09-949-016-17420
;  Sequence 17420, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17420
;  LENGTH: 84571
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(84571)
;  OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17420

Query Match    49.6%;  Score 169.8;  DB 3;  Length 84571;
Best Local Similarity   49.6%;
Matches  571;  Conservative  0;  Mismatches  547;  Indels  33;  Gaps  4;

Qy      833 TAAGAGGAGGAGGACATAATAGTGGATTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTA 892
            || | ||| | ||| |   ||||| | ||| ||||||| | | ||  |||| | ||| || |||
Db    80762 TAGAACAAGGACTGCTGGTAAAGGAAGAACTTAAAACTCATAAAATATAAAATCCAAACT 80821

Qy      893 CAAAATTTCAGTTGGATGTGCCATCAATAATACCATTGATAATTGCTACCTCTCTTG 952
            |||||||| ||||||||| | |||| |  || |||||  || || ||| | | |||
Db    80822 TGCAATTTAAACTTGATGTTCTGTCACTGATACCAACTGATTTGCTGTATTTTAAGTTAG 80881

Qy      953 GGTTTA---ATCCAAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCATTTTTGAAT 1009
            || ||    |||||| || | |||||||||| |  ||| | | |||| |||||| || |
Db    80882 GGTGGAACTATCCAGAAATTAGATTAACAGGTTGTTACGGTTCTTCGTATGTTTGAGT 80941

Qy     1010 TTAATCATCACCTGAGTCTATAATGGACAAAGCATATATCTACACAGAGTTATTCGAACA 1069
            || |  |||| || |  || ||||||||| | || || ||| | ||||| |  ||||||
Db    80942 TCTTCCAGAAACAGAAACAGAAACAAGGACAAACTATCCAAACATCTTCAGGATTTCCAACCTTG 81001

Qy     1070 CTGGATACTTGCTGTTTATTCTGCACATTAATGCCTGTGTTTATTACTGGGCTTCAAAACT 1129
            |||| |  |||||| || |||  |||||| || ||||||| ||||  ||| | ||||| |
Db    81002 TTATGTATACGTCATCATTATCCACTGAATGCACATGTGTGTTTATTACTCTATTTCTAAAG 81061
```

RESULT 13
US-09-949-016-38897/c
; Sequence 38897, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 38897
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38897

Query Match   6.2%; Score 151.4; DB 3; Length 601;
Best Local Similarity 99.3%; Pred. No. 2.4e-27;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 493 GCAAAGCCCACGGCTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTAC 552
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 291 GCAAAGCCCACGGCTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTAC 232

Qy 553 TACAGGCGTTGTTGGTTCAAAAGTCAAAAAGATCCCTTTTAACAGAGTACTTAAAGCGAATT 612
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 231 TACAGGCGTTGTTGGTTCAAAAGTCAAAAAGATCCCTTTTAACAGAGTACTTAAAGCGAATT 172

Qy 613 AAACTTCCAAACAGCATAGATTCATACACAGAT 645
         |||||||||||||||||||||||||||||||||
Db 171 AAACTTCCAAACAGCATAGATTCATACACAGGT 139

RESULT 14
US-09-949-016-205175/c
; Sequence 205175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 205175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205175

Query Match   6.2%; Score 151.4; DB 3; Length 601;
Best Local Similarity 99.3%; Pred. No. 2.4e-27;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 493 GCAAAGCCCACGGCTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTAC 552
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 291 GCAAAGCCCACGGCTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTAC 232

Qy 553 TACAGGCGTTGTTGGTTCAAAAGTCAAAAAGATCCCTTTTAACAGAGTACTTAAAGCGAATT 612
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 231 TACAGGCGTTGTTGGTTCAAAAGTCAAAAAGATCCCTTTTAACAGAGTACTTAAAGCGAATT 172

Qy 613 AAACTTCCAAACAGCATAGATTCATACACAGAT 645
         |||||||||||||||||||||||||||||||||
Db 171 AAACTTCCAAACAGCATAGATTCATACACAGGT 139

Qy 1130 ATGAAGGAAATTGGCACTACTACGAATGGGTGTA--------------------TGATG 1165
          |||||||||||| |||||
Db 81062 CTATTGGATTTGGAAATGATGACAGTGGGTGTCACCCTGATATATTAATTACCATTG 81121

Qy 1166 GGGAAGGAAAACGAGTATCTGAGGATGTTATTATTGGGGCAGTTCGAACTTTAATTACCATTG 1225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81122 GTTTTGGCTAGAAAATAAGTATACAGCCTTTACTGGTCTTACTGACTTTGACTACCATTG 81181

Qy 1226 GTGGCCTTCCAGAACCACACAAACTTTATTTGAAAATTGTTTTTCAAACTCTTGAATTTTTTT 1285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81182 GTGAAAACACCCCTCCCGTGAGGGAATTCTGAGTATGTCTTTGTGGTGGTTGATTCCTAA 81241

Qy 1286 CTGGAGTTTTTGTGTTCTCCACTTTAATTGGTTCAGATGAGGAGATGTGATTGGAGCAGCTA 1345
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81242 TTGGAGTGTTTAATTTTTTGCTACCATCGTTGGTTAACATAGGTTCTATGATTCCAACATGA 81301

Qy 1346 CAGCCAATCAGAACTACTTCCGCGGCCTTGCACATGGATGACACCATTGCCTACTACCGCTTG 1405
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81302 ATGCAGCCAGAGCAGAATTTCAAGCAAGAAATTGATGCTTATCAAGCAATATATGCATTTTC 81361

Qy 1406 ACTCCATTCCTAAACTTGTGCAAAAAAGGGAGTTCGGACTTGGGTATGAAATATACATGGGACT 1465
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81362 GAAATGTAAGCAAAGATATGGAAAAAGAGGGTTATTGAAGGTTTGACTACCTGTGGACCA 81421

Qy 1466 CTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAGACCCTACCAACTACGGGTCCAGTTAG 1525
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81422 ACAAAAAAACAGTTGATGAGAAAGAGTCTTAAAGTATCTACCTGATAAAAACTAAGAGCAG 81481

Qy 1526 CCCTCGCCATTGATGTGAAACTTCAGCAATCATCAGCAAAGTCGACTTGTTCAAGGGTTGTG 1585
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81482 AAAATTGCCATCAAACGTTCACTTAGACACATTAAAAAAGGTACGACCATTTTTGCTGATTGTG 81541

Qy 1586 ATACACAGATGATTTATGACATGTTGCTAAGATTGAAAATCCGTTCTCTCTTATTTGCCTGGTG 1645
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81542 AAGCTGGTCTGTTGGTGGTCTTGAAATTGCAACCCCAAGTCTACAGTCCTGGAC 81601

Qy 1646 ACTTTGTCTGCAAAAAGGGAGAAATTGGCAAGGAGAAATGTATATCATCAAGCATGGAGAAG 1705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81602 ATTATATTTGCAAGAAAAAGGGGGATTATCGGACGAGAGAGATGTACATTATCAAGGAAGGCAAAC 81661

Qy 1706 TCCAAGTTCTTGGGAGGCGCCTGAGTGGTACTAAAGTTCTGGGT----TACTTCTGAAAGTCTGGG 1761
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db 81662 TCGCTGTGGGTGGCGATGATGGAGTCACTCAGTTTGTGTGCTACTAATGCCGATGGCAGCTACT 81721

Qy 1762 TCGGTGTTTGGGAGAAAATC--AGCCTTCTTAGCACGCAGGAGGAGGAGAAACCGTCGAACTCGCCA 1819
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db 81722 TCGGTGAGATCAGCATTCTTAACATTAAAAGGGAGCAAAAGCTTGGCAATCGAAGAAACGGCCA 81781

Qy 1820 ATGTGGTGGGCCCACGGGGTTTGCCAATCTTTTTAACTCTAGAACACAAAGACCCTCCAAGAA 1879
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81782 ATATTAAAAAGTATTGGGCTTGTTACTCAGACCTTGTCTCTCAAAAGATGACCTCCATGGAAG 81841

Qy 1880 TTCTTAGTTGTCATTATATCCAGATTCTCATTGGAAAAGGGATCCTCATGAGAAAAGCCAGAGTTGCTTTTAA 1939
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81842 CTCTAACTGAGTGTACCCAGATGCCAAAACTATCCTGGAAGAGAAAAGGGAGCGACAGATTTTAA 81901

Qy 1940 ACCAGAAGGCT 1950
          |||||||||||
Db 81902 TGAAAGATGGT 81912

RESULT 15
US-09-949-016-38915/c
; Sequence 38915, Application US/09949016
; Patent No. 6812239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig, et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38915
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38915

Query Match   6.1%; Score 147.6; DB 3; Length 601;
Best Local Similarity   97.4%; Pred. No. 2.1e-26;
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   1336 GGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTAC 1395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTAC 542

Qy   1396 ATGAACAATTACTCCATTCCTAAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATAT 1455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 ATGAACAATTACTCCATTCCTAAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATAT 482

Qy   1456 ACATGGGGACTCTCAAAGAATGCTAGATGAGTCTG 1489
           ||||||||||||||||||||||||||||||||||
Db   481 ACATGGGGACTCTCAAAGAATGCTAGGTAAGCATG 448

Search completed: May 19, 2006, 02:11:03
Job time : 825 secs

This Page Blank (uspto)